

82028

From: Salimi, Ali  
Sent: Tuesday, December 10, 2002 1:52 PM  
To: STIC-Biotech/ChemLib  
Subject: 09/701,080

Can you please conduct a search for the application serial no. 09/701,080, including interference search for the following sequences:

SEQ ID NO: 1, and 18

Thanks!

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AU 1648  
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Edward Hart  
Technical Info. Specialist  
STIC/Biotech  
CMI 6B02 Tel: 305-9203

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 12/13/02  
Date Completed: 12/13/02  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:

NA Sequences: \_\_\_\_\_  
AA Sequences: 2  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: 02  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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QY 1 MFQDPQERPKLPQLCTELQTTIHDIILECVYCKQQLRRREYDFAFRDLCIVYRDGPNY 60

```
Db      8 MFODPOERPRKLPOLCTELQTTIHDIILECVYCKQOLLREVVDFAFRDLCIYRDGNPY 67
QY      61 AVCDKCLKFSKYSERYHVCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 120
Db      68 AVCDKCLKFSKYSERYHVCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 127
QY      121 KQRFNHNIRGRWTRGCMSCCRSSSTRRETOL 151
Db      128 KQRFNHNIRGRWTRGCMSCCRSSSTRRETOL 158

RESULT 2
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PNO157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match          99.1%; Score 843; DB 3; Length 266;
Best Local Similarity 99.3%; Pred. No. 4,9e-82;
Matches 150; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 MFODPOERPRKLPOLCTELQTTIHDIILECVYCKQOLLREVVDFAFRDLCIYRDGNPY 60
Db      8 MFODPOERPRKLPOLCTELQTTIHDIILECVYCKQOLLREVVDFAFRDLCIYRDGNPY 67
QY      61 AVCDKCLKFSKYSERYHVCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 120
Db      68 AVCDKCLKFSKYSERYHVCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 127
QY      121 KQRFNHNIRGRWTRGCMSCCRSSSTRRETOL 151
Db      128 KQRFNHNIRGRWTRGCMSCCRSSSTRRETOL 158

RESULT 3
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
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; EARLIER APPLICATION NUMBER: AU PNO157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRF
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match          99.1%; Score 843; DB 4; Length 266;
Best Local Similarity 99.3%; Pred. No. 4,9e-82;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MFODPOERPRKLPOLCTELQTTIHDIILECVYCKQOLLREVVDFAFRDLCIYRDGNPY 60
Db      8 MFODPOERPRKLPOLCTELQTTIHDIILECVYCKQOLLREVVDFAFRDLCIYRDGNPY 67
QY      61 AVCDKCLKFSKYSERYHVCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 120
Db      68 AVCDKCLKFSKYSERYHVCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 127
QY      121 KQRFNHNIRGRWTRGCMSCCRSSSTRRETOL 151
Db      128 KQRFNHNIRGRWTRGCMSCCRSSSTRRETOL 158

RESULT 4
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRF
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match          99.1%; Score 843; DB 4; Length 266;
Best Local Similarity 99.3%; Pred. No. 4,9e-82;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MFODPOERPRKLPOLCTELQTTIHDIILECVYCKQOLLREVVDFAFRDLCIYRDGNPY 60
Db      8 MFODPOERPRKLPOLCTELQTTIHDIILECVYCKQOLLREVVDFAFRDLCIYRDGNPY 67
QY      61 AVCDKCLKFSKYSERYHVCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 120
Db      68 AVCDKCLKFSKYSERYHVCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 127
QY      121 KQRFNHNIRGRWTRGCMSCCRSSSTRRETOL 151
Db      128 KQRFNHNIRGRWTRGCMSCCRSSSTRRETOL 158

RESULT 5
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
```



Query Match	99.1%	Score 843;	DB 4;	Length 292;
Best Local Similarity	99.3%;	Fred. No.5.4e-82;		
Matches 150;	Conservative	0;	Mismatches 1;	Indels 0;
Gaps	0;			
QY	1	MFQDQERPRKIPQCTETQTTIHIIILCEVCYCKQOLLREYVDEAFRLCIAYRDNQNY	60	
DB	133	MFQDQERPRKIPQCTETQTTIHIIILCEVCYCKQOLLREYVDEAFRLCIAYRDNQNY	192	
QY	61	AVCDKCLKFSYSEYRHYCYSLYGTTLQEQYNNKPLCDLLIRCIHQCPFLCPPEKORHLD	120	

```

/ RESULT 8
/ US-09-485-885-14
/ Sequence 14 Application US/09485885
/ Patent No. 6342224
/ GENERAL INFORMATION:
/ APPLICANT: Bruck, Claudine
/ APPLICANT: Cabezon Silva, Teresa
/ APPLICANT: Delisse, Anne-Marie Eva Fernandez
/ APPLICANT: Gerard, Catherine Marie Ghislaine
/ APPLICANT: Lombardo-Bencheikh, Angela
/ TITLE OF INVENTION: Vaccine
/ FILE REFERENCE: B45107
/ CURRENT APPLICATION NUMBER: US/09/485,885
/ CURRENT FILING DATE: 2000-02-18
/ PRIOR APPLICATION NUMBER: PCT/EP98/05285
/ PRIOR FILING DATE: 1998-08-17
/ PRIOR APPLICATION NUMBER: GB 9717953.5
/ PRIOR FILING DATE: 1997-08-22
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: FASTSEQ for Windows Version 3.0
/ SEQ ID NO 14
/ LENGTH: 390
/ TYPE: PRT
/

```

ORGANISM: Homo sapien  
US-09-485-885-14

Query Match  
Best Local Similarity 99.1%; Score 843; DB 4; Length 390;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKOQLLRREYVDFAFRDLCIYRGDGNPY 60  
DB 133 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKOQLLRREYVDFAFRDLCIYRGDGNPY 192  
QY 61 AVCDCKLKFYSKISEYRHYCYSLYGTLLLEQYKPKLDDLIRINCOKPLCPPEKORHLD 120  
DB 193 AVCDCKLKFYSKISEYRHYCYSLYGTLLLEQYKPKLDDLIRINCOKPLCPPEKORHLD 252  
QY 121 KROFHNIRGRWTRGCMSCCRSSRTREYOL 151  
DB 253 KROFHNIRGRWTRGCMSCCRSSRTREYOL 283

## RESULT 9

US-08-316-239B-4  
Sequence 4, Application US/08316239B  
Patent No. 5679509

GENERAL INFORMATION:  
APPLICANT: Wheeler, Cosette M.  
APPLICANT: Parmenter, Cheryl A.  
TITLE OF INVENTION: Methods and a Diagnostic Aid for  
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an  
TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and  
TITLE OF INVENTION: Cervical Cancer  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jagtiani & Associates  
STREET: 6126 Rocky Way Court  
CITY: Centerville  
STATE: VA  
COUNTRY: USA  
ZIP: 20120-3400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/316,239B  
FILING DATE: 30-SEP-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Jagtiani, Ajay A.  
REGISTRATION NUMBER: 35,205  
REFERENCE/DOCKET NUMBER: UNME-0001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 817-9453  
TELEFAX: (703) 803-9387  
INFORMATION FOR SEQ. ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 162 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-08-316-239B-4

Query Match  
Best Local Similarity 98.7%; Score 840; DB 1; Length 162;  
Matches 149; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKOQLLRREYVDFAFRDLCIYRGDGNPY 60  
DB 8 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKOQLLRREYVDFAFRDLCIYRGDGNPY 67

QY 61 AVCDCKLKFYSKISEYRHYCYSLYGTLLLEQYKPKLDDLIRINCOKPLCPPEKORHLD 120  
DB 68 AVCDCKLKFYSKISEYRHYCYSLYGTLLLEQYKPKLDDLIRINCOKPLCPPEKORHLD 127  
QY 121 KROFHNIRGRWTRGCMSCCRSSRTREYOL 151  
DB 128 KROFHNIRGRWTRGCMSCCRSSRTREYOL 158

## RESULT 10

US-08-860-165-12  
Sequence 12, Application US/08860165A  
Patent No. 6004557

GENERAL INFORMATION:  
APPLICANT: EDWARDS, Stirling John  
APPLICANT: COX, John Cooper  
APPLICANT: WEBB, Elizabeth Ann  
APPLICANT: FRAZER, Ian  
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS  
FILE REFERENCE: 17227/130  
CURRENT APPLICATION NUMBER: US/08/860,165A  
EARLIER FILING DATE: 1997-09-22  
EARLIER APPLICATION NUMBER: PCT/AU95/00868  
EARLIER FILING DATE: 1995-12-20  
EARLIER APPLICATION NUMBER: AU PNO157  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO: 12  
LENGTH: 172  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion  
US-08-860-165-12

Query Match  
Best Local Similarity 63.3%; Score 539; DB 3; Length 172;  
Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 57 GNPYAVCDCKLKFYSKISEYRHYCYSLYGTLLLEQYKPKLDDLIRINCOKPLCPPEKOR 116  
DB 2 GNPYAVCDCKLKFYSKISEYRHYCYSLYGTLLLEQYKPKLDDLIRINCOKPLCPPEKOR 61  
QY 117 RHLDKKROFHNIRGRWTRGCMSCCRSSRTREYOL 151  
DB 62 RHLDKKROFHNIRGRWTRGCMSCCRSSRTREYOL 96

## RESULT 11

US-09-359-382-12  
Sequence 12, Application US/09359382  
Patent No. 6306397

GENERAL INFORMATION:  
APPLICANT: EDWARDS, Stirling John  
APPLICANT: COX, John Cooper  
APPLICANT: WEBB, Elizabeth Ann  
APPLICANT: FRAZER, Ian  
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS  
FILE REFERENCE: 017227/0148  
CURRENT APPLICATION NUMBER: US/09/359,382  
EARLIER FILING DATE: 1999-07-23  
EARLIER APPLICATION NUMBER: US 08/860,165  
EARLIER FILING DATE: 1997-09-22  
EARLIER APPLICATION NUMBER: PCT/AU95/00868  
EARLIER FILING DATE: 1995-12-20  
EARLIER APPLICATION NUMBER: AU PNO157/94  
EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO: 12  
LENGTH: 172  
TYPE: PRT

```
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match          63.3%; Score 539; DB 4; Length 172;
Best Local Similarity 98.9%; Pred. No. 5,9e-50;
Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 57 GNPYAVCDKCLKFKYSKYSEYRHYCYSLYGTTLLEQOYNKPLCDLLIRJCINQKPLCPPEKO 116
      |||
DB 2 GNPYAVCDKCLKFKYSKYSEYRHYCYSLYGTTLLEQOYNKPLCDLLIRJCINQKPLCPPEKO 61

QY 117 RHLDKKRFHNIRGRTGRCMSSCRSSRTRETOL 151
      |||
DB 62 RHLDKKRFHNIRGRTGRCMSSCRSSRTRETOL 96

RESULT 12
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match          57.2%; Score 487; DB 3; Length 172;
Best Local Similarity 93.5%; Pred. No. 2e-44;
Matches 87; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFQDDPERPRKLPQLCTELQTTIHDIILLCYCKQOLLRREYVDFAFRDLCTIYVRDGNPY 60
      |||
DB 77 MFQDDPERPRKLPQLCTELQTTIHDIILLCYCKQOLLRREYVDFAFRDLCTIYVRDGNPY 136

QY 61 AVCDKCLKFKYSKYSEYRHYCYSLYGTTLLEQOYN 93
      |||
DB 137 AVCDKCLKFKYSKYSEYRHYCYSLYGTTLRSHHH 169

RESULT 13
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; EARLIER FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
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; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match          57.2%; Score 487; DB 4; Length 172;
Best Local Similarity 93.5%; Pred. No. 2e-44;
Matches 87; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFQDDPERPRKLPQLCTELQTTIHDIILLCYCKQOLLRREYVDFAFRDLCTIYVRDGNPY 60
      |||
DB 77 MFQDDPERPRKLPQLCTELQTTIHDIILLCYCKQOLLRREYVDFAFRDLCTIYVRDGNPY 136

QY 61 AVCDKCLKFKYSKYSEYRHYCYSLYGTTLLEQOYN 93
      |||
DB 137 AVCDKCLKFKYSKYSEYRHYCYSLYGTTLRSHHH 169

RESULT 14
US-08-117-083-10
; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Bourisnell, Michael E.
; APPLICANT: Ingils, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: A35
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-368-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1,182
; OTHER INFORMATION: /note="Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
US-08-117-083-10

Query Match          56.3%; Score 479; DB 1; Length 182;
```



```

ID  AAY02633 standard; Protein: 371 AA.
XX
AC  AAY02633;
XX
DT  22-JUN-1999 (first entry)
XX
DE  Prot.D1/3-E6-E7-His/HPV16 protein.
XX
KM  Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;
XX  tumour; lesion; benign; malignant; virus; infection.
XX
OS  Chimeric - Human papillomavirus.
XX  Chimeric - Haemophilus influenzae.
XX
PN  W0910375-A2.
XX
PD  04-MAR-1999.
XX
PF  17-AUG-1998; 98WO-EP05285.
XX
PR  22-AUG-1997; 97GB-0017953.
XX
PA  (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI  Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;
XX  Lombardo-Bencheikh A;
XX
DR  WPI: 1999-190587/16.
XX  N-PSDB; AAX29782.
XX
PT  Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
XX  treatment or prophylaxis of HPV induced lesions
XX
PS  Disclosure; Fig 6; 95pp; English.
XX
CC  This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion
XX  protein from Human papillomavirus (HPV) linked to an immunological fusion
XX  partner, in this case, a fragment of the Haemophilus influenzae B
XX  protein D. The sequence also contains a histidine tag at the C-terminus
XX  of the encoded protein. The protein can be used in a vaccine, for
XX  immuno-therapeutically treating HPV induced tumour lesions (benign or
XX  malignant) and preventing HPV viral infection.
XX
SQ  Sequence 371 AA;

Query Match 99.1%; Score 843; DB 20; Length 371;
Best Local Similarity 99.3%; Pred. No. 2.7e-82;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREVDFAFRDLCIYRDGNPY 60
    |||||||
DB 114 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREVDFAFRDLCIYRDGNPY 173

QY 61 AVCDKCLKFYSKYSEYRHGYSLYGTLEDOYKNPLCDLLIRICINCKPILCPPEKORHLD 120
    |||||||
DB 174 AVCDKCLKFYSKYSEYRHGYSLYGTLEDOYKNPLCDLLIRICINCKPILCPPEKORHLD 233

QY 121 KKQRFHNIRGHWGRCMSSCRSSRTRETOL 151
    |||||||
DB 234 KKQRFHNIRGHWGRCMSSCRSSRTRETOL 264

RESULT 15
AAY25381
ID  AAY25381 standard; Protein: 390 AA.
XX
AC  AAY25381;
XX
DT  06-SEP-1999 (first entry)
XX
DE  HPV fusion protein CLYTA-E6E7-His/HPV16.
XX
KM  Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
XX

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```

KM  Immunological fusion partner; CpG oligonucleotide; immune response;
XX  HPV antigen; prevention; treatment.
XX
OS  Synthetic.
XX  Human papillomavirus.
XX
PN  W0933868-A2.
XX
PD  08-JUL-1999.
XX
PF  18-DEC-1998; 98WO-EP08563.
XX
PR  24-DEC-1997; 97GB-0027262.
XX
PA  (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI  Dalemans WLJ, Gerard CMG;
XX
DR  WPI: 1999-405485/34.
XX  N-PSDB; AAX78797.
XX
PT  Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
XX  induce immune response to HPV
XX
PS  Example VII; Page 55-56; 62pp; English.
XX
CC  AAX78791-X78801 represent nucleic acid sequences which encode novel
XX  constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
XX  HPV (represented in AAY25375-Y25386). These constructs are optionally
XX  linked to an immunological fusion partner and an immunomodulatory CpG
XX  oligonucleotide. The products of the invention can be used to induce an
XX  immune response in a patient to an HPV antigen. They can also be used
XX  for preventing or treating HPV induced tumours.
XX
SQ  Sequence 390 AA;

Query Match 99.1%; Score 843; DB 20; Length 390;
Best Local Similarity 99.3%; Pred. No. 2.9e-82;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREVDFAFRDLCIYRDGNPY 60
    |||||||
DB 133 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREVDFAFRDLCIYRDGNPY 192

QY 61 AVCDKCLKFYSKYSEYRHGYSLYGTLEDOYKNPLCDLLIRICINCKPILCPPEKORHLD 120
    |||||||
DB 193 AVCDKCLKFYSKYSEYRHGYSLYGTLEDOYKNPLCDLLIRICINCKPILCPPEKORHLD 252

QY 121 KKQRFHNIRGHWGRCMSSCRSSRTRETOL 151
    |||||||
DB 253 KKQRFHNIRGHWGRCMSSCRSSRTRETOL 283

Search completed: December 13, 2002, 08:38:15
Job time : 60.362 secs

```

Query Match 99.1%; Score 843; DB 20; Length 292;  
 Best Local Similarity 99.3%; Pred. No. 2.1e-82;  
 Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFQDPQRPRLPOLCTELQTTHTDITLLECYCKQQLLRREYVDFAFRDLCTIYRDGNPY 60  
 |||||||  
 DB 133 MFQDPQRPRLPOLCTELQTTHTDITLLECYCKQQLLRREYVDFAFRDLCTIYRDGNPY 192

QY 61 AVCDKCLKFSKSEYRHVCYSLYGTTLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 120  
 |||||||  
 DB 193 AVCDKCLKFSKSEYRHVCYSLYGTTLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 252

QY 121 KQRFHNRGRWTRGCMSCCRSSRTRETQL 151  
 |||||||  
 DB 253 KQRFHNRGRWTRGCMSCCRSSRTRETQL 283

RESULT 12  
 AAY02635  
 ID AAY02635 standard; Protein: 292 AA.  
 AC AAY02635;  
 XX  
 DT 22-JUN-1999 (first entry)  
 XX  
 DE CLYTA-E6-His protein.  
 XX  
 KM Chimeric; E6; E7; fusion protein; CLYTA; vaccine; immunotherapy;  
 KM tumour; lesion; benign; malignant; virus; infection.  
 XX  
 OS Chimeric - Human papillomavirus.  
 OS Chimeric - Streptococcus pneumoniae.  
 XX  
 PN MO9910375-A2.  
 XX  
 PD 04-MAR-1999.  
 XX  
 PF 17-AUG-1998; 98WO-EP05285.  
 XX  
 PR 22-AUG-1997; 97GB-0017953.  
 XX  
 PA (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;  
 PI Lombardo-Benchelkh A;  
 PI  
 DR WPI; 1999-190587/16.  
 DR N-PSDB; AAX29784.  
 XX  
 PT Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for  
 PT treatment or prophylaxis of HPV induced lesions  
 XX  
 PS Disclosure; Fig 10; 95pp; English.  
 XX  
 CC This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion  
 CC protein from Human papillomavirus (HPV) linked to an immunological fusion  
 CC partner, in this case, a fragment of the Streptococcus pneumoniae CLYTA  
 CC protein of the encoded protein. The protein can be used in a vaccine,  
 CC for immuno-therapeutically treating HPV induced tumour lesions (benign  
 CC or malignant) and preventing HPV viral infection.  
 CC  
 SQ Sequence 292 AA;

Query Match 99.1%; Score 843; DB 20; Length 292;  
 Best Local Similarity 99.3%; Pred. No. 2.1e-82;  
 Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFQDPQRPRLPOLCTELQTTHTDITLLECYCKQQLLRREYVDFAFRDLCTIYRDGNPY 60  
 |||||||  
 DB 133 MFQDPQRPRLPOLCTELQTTHTDITLLECYCKQQLLRREYVDFAFRDLCTIYRDGNPY 192

QY 61 AVCDKCLKFSKSEYRHVCYSLYGTTLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 120  
 |||||||  
 DB 193 AVCDKCLKFSKSEYRHVCYSLYGTTLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 252

DB 193 AVCDKCLKFSKSEYRHVCYSLYGTTLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 252

QY 121 KQRFHNRGRWTRGCMSCCRSSRTRETQL 151  
 |||||||  
 DB 253 KQRFHNRGRWTRGCMSCCRSSRTRETQL 283

RESULT 13  
 AAY25377  
 ID AAY25377 standard; Protein: 371 AA.  
 AC AAY25377;  
 XX  
 DT 06-SEP-1999 (first entry)  
 XX  
 DE HPV fusion protein DI/3-E6E7-His/HPV16.  
 XX  
 KM Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;  
 KM immunological fusion partner; Cpg oligonucleotide; immune response;  
 KM HPV antigen; prevention; treatment.  
 XX  
 OS Synthetic.  
 OS Human papillomavirus.  
 XX  
 PN WO933868-A2.  
 XX  
 PD 08-JUL-1999.  
 XX  
 PF 18-DEC-1998; 98WO-EP08563.  
 XX  
 PR 24-DEC-1997; 97GB-0027262.  
 XX  
 PA (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA Dalemans WLJ, Gerard CMG;  
 PI  
 DR WPI; 1999-405485/34.  
 DR N-PSDB; AAX78793.  
 XX  
 PT Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to  
 PT induce immune response to HPV  
 XX  
 PS Example III; Page 50; 62pp; English.  
 XX  
 CC AAX78791-X78801 represent nucleic acid sequences which encode novel  
 CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from  
 CC HPV (represented in AAY25375-Y25386). These constructs are optionally  
 CC linked to an immunological fusion partner and an immunomodulatory Cpg  
 CC oligonucleotide. The products of the invention can be used to induce an  
 CC immune response in a patient to an HPV antigen. They can also be used  
 CC for preventing or treating HPV induced tumours.  
 CC  
 SQ Sequence 371 AA;

Query Match 99.1%; Score 843; DB 20; Length 371;  
 Best Local Similarity 99.3%; Pred. No. 2.7e-82;  
 Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFQDPQRPRLPOLCTELQTTHTDITLLECYCKQQLLRREYVDFAFRDLCTIYRDGNPY 60  
 |||||||  
 DB 114 MFQDPQRPRLPOLCTELQTTHTDITLLECYCKQQLLRREYVDFAFRDLCTIYRDGNPY 173

QY 61 AVCDKCLKFSKSEYRHVCYSLYGTTLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 120  
 |||||||  
 DB 174 AVCDKCLKFSKSEYRHVCYSLYGTTLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 233

QY 121 KQRFHNRGRWTRGCMSCCRSSRTRETQL 151  
 |||||||  
 DB 234 KQRFHNRGRWTRGCMSCCRSSRTRETQL 264

RESULT 14  
 AAY02633

DR WPI; 1999-405485/34.  
 DR N-PSDB; AAX78792.  
 XX  
 PT Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to  
 PT induce immune response to HPV  
 XX  
 PS Example II; Page 48-49; 62pp; English.  
 XX  
 CC AAX78791-X78801 represent nucleic acid sequences which encode novel  
 CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from  
 CC HPV (represented in AAY25375-Y25386). These constructs are optionally  
 CC linked to an immunological fusion partner and an immunomodulatory CpG  
 CC oligonucleotide. The products of the invention can be used to induce an  
 CC immune response in a patient to an HPV antigen. They can also be used  
 CC for preventing or treating HPV induced tumours.  
 XX  
 SQ Sequence 273 AA;  
 Query Match 99.1%; Score 843; DB 20; Length 273;  
 Best Local Similarity 99.3%; Pred. No. 1.9e-82;  
 Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MFODPQRPRLPQLCTELQTTIHDIIECYCKQQLLRREYDFARFDCIYRQGNPY 60  
 DB 114 MFODPQRPRLPQLCTELQTTIHDIIECYCKQQLLRREYDFARFDCIYRQGNPY 173  
 QY 61 AVCDKCLFYSKYSEYRHYCYSLYGTTLLEOYNNKPLCDLLIRICINCKPLCPPEKORHLD 120  
 DB 174 AVCDKCLFYSKYSEYRHYCYSLYGTTLLEOYNNKPLCDLLIRICINCKPLCPPEKORHLD 233  
 QY 121 KKQRFHNIIRGWTGRMCCSCRSSRRTRETOL 151  
 DB 234 KKQRFHNIIRGWTGRMCCSCRSSRRTRETOL 264  
 RESULT 10  
 AAY02632  
 ID AAY02632 standard; Protein; 273 AA.  
 XX  
 AC AAY02632;  
 XX  
 DT 22-JUN-1999 (first entry)  
 XX  
 DE Prot.D1/3-E6-His/HPV16 protein.  
 XX  
 KW Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;  
 KW tumour; lesion; benign; malignant; virus; infection.  
 XX  
 OS Chimeric - Human papillomavirus.  
 OS Chimeric - Haemophilus influenzae.  
 XX  
 PN WO910375-A2.  
 XX  
 PD 04-MAR-1999.  
 XX  
 PF 17-AUG-1998; 98WO-EP05285.  
 XX  
 PR 22-AUG-1997; 97GB-0017953.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;  
 PI Lombardo-Bencheikh A;  
 XX  
 DR WPI; 1999-190587/16.  
 DR N-PSDB; AAX29781.  
 XX  
 PT Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for  
 PT treatment or prophylaxis of HPV induced lesions  
 XX  
 PS Disclosure; Fig 3; 95pp; English.  
 CC This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion

CC protein from Human papillomavirus (HPV) linked to an immunological fusion  
 CC partner, in this case, a fragment of the Haemophilus influenzae B  
 CC protein D. The sequence also contains a histidine tag at the C-terminus  
 CC of the encoded protein. The protein can be used in a vaccine, for  
 CC immuno-therapeutically treating HPV induced tumour lesions (benign or  
 CC malignant) and preventing HPV viral infection.  
 XX  
 SQ Sequence 273 AA;  
 Query Match 99.1%; Score 843; DB 20; Length 273;  
 Best Local Similarity 99.3%; Pred. No. 1.9e-82;  
 Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MFODPQRPRLPQLCTELQTTIHDIIECYCKQQLLRREYDFARFDCIYRQGNPY 60  
 DB 114 MFODPQRPRLPQLCTELQTTIHDIIECYCKQQLLRREYDFARFDCIYRQGNPY 173  
 QY 61 AVCDKCLFYSKYSEYRHYCYSLYGTTLLEOYNNKPLCDLLIRICINCKPLCPPEKORHLD 120  
 DB 174 AVCDKCLFYSKYSEYRHYCYSLYGTTLLEOYNNKPLCDLLIRICINCKPLCPPEKORHLD 233  
 QY 121 KKQRFHNIIRGWTGRMCCSCRSSRRTRETOL 151  
 DB 234 KKQRFHNIIRGWTGRMCCSCRSSRRTRETOL 264  
 RESULT 11  
 AAY25379  
 ID AAY25379 standard; Protein; 292 AA.  
 XX  
 AC AAY25379;  
 XX  
 DT 06-SEP-1999 (first entry)  
 XX  
 DE HPV fusion protein CLYTA-E6-His/HPV16.  
 XX  
 KW Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;  
 KW immunological fusion partner; CpG oligonucleotide; immune response;  
 KW HPV antigen; prevention; treatment.  
 XX  
 OS Synthetic.  
 OS Human papillomavirus.  
 XX  
 PN WO9933868-A2.  
 XX  
 PD 08-JUL-1999.  
 XX  
 PF 18-DEC-1998; 98WO-EP08563.  
 XX  
 PR 24-DEC-1997; 97GB-0027262.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Dalemans WLJ, Gerard CMG;  
 PI  
 XX  
 DR WPI; 1999-405485/34.  
 DR N-PSDB; AAX78795.  
 XX  
 PT Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to  
 PT induce immune response to HPV  
 XX  
 PS Example VI; Page 52-53; 62pp; English.  
 XX  
 CC AAX78791-X78801 represent nucleic acid sequences which encode novel  
 CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from  
 CC HPV (represented in AAY25375-Y25386). These constructs are optionally  
 CC linked to an immunological fusion partner and an immunomodulatory CpG  
 CC oligonucleotide. The products of the invention can be used to induce an  
 CC immune response in a patient to an HPV antigen. They can also be used  
 CC for preventing or treating HPV induced tumours.  
 XX  
 SQ Sequence 292 AA;

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XX 14-MAR-1991: 91GB-0005383.
XX
XX (IMMU ) IMMUNOLOGY LTD.
XX
XX Boursnell MEG, Inglis SC, Munro AJ;
XX
XX WPI; 1992-349219/42.
XX
XX N-PSDB; AAQ29389.
XX
XX Recombinant virus vectors encoding human papillomavirus proteins
XX - for treating and vaccinating against HPV infections and
XX conditions caused by them, such as cervical cancer
XX
XX
XX PS Disclosure; Fig 1a; 83pp; English.
XX
XX The fragment of DNA contg. the HPV-16 E6/E7 coding region was
XX prep'd. by PCR from plasmid pBR322/HPV16 (Durst et al., PNAS, 80:
XX 3812 (1983)) using oligonucleotides S05 and S06. The prod. of the
XX third reading frame is the HPV-16 E6 protein whereas the second
XX reading frame encodes HPV-16 E7. The E6 and E7 ORFs are fused
XX together to form a single continuous ORF via site directed mutagenesis
XX and the immortalising potential of E7 is removed by altering two key
XX codons of the HPV E7 sequence. The single ORF of HPV-16 E6/E7 may be
XX inserted into vaccinia virus DNA at neutral sites (pref. by inserting
XX two sets of the DNA in opposite orientations to overcome the problem
XX of intertypic recombination) to make a recombinant virus vector for
XX use immunotherapeutically to activate cells of the immune system
XX against HPV. See also AAR27723-43.
XX
XX SQ Sequence 263 AA;
XX
XX Query Match 99.1%; Score 843; DB 13; Length 263;
XX Best Local Similarity 99.3%; Pred. No. 1.8e-82;
XX Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCIYVRDGNPY 60
XX |
XX DB 9 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCIYVRDGNPY 68
XX
XX QY 61 AVCDKCLKFYSKYSEYRHYCYSLYGTTLDEQYKKPLCDLLIRINCQKPLCPBEKQRHLD 120
XX |
XX DB 69 AVCDKCLKFYSKYSEYRHYCYSLYGTTLDEQYKKPLCDLLIRINCQKPLCPBEKQRHLD 128
XX
XX QY 121 KQRFNINIRGRTGRCMSCCRSSRTRETQL 151
XX |
XX DB 129 KQRFNINIRGRTGRCMSCCRSSRTRETQL 159
XX
XX RESULT 8
XX AAR97561
XX ID AAR97561 standard; Protein; 266 AA.
XX
XX AC AAR97561;
XX
XX 11-JAN-1997 (first entry)
XX
XX DE Human papilloma virus E6/E7 protein variant.
XX
XX KW Human papilloma virus; E6; E7; deletion mutant; HPV;
XX immune response; humoral immune response; cellular immune response;
XX vaccine.
XX
XX OS Human papilloma virus.
XX
XX PN WO9619496-A1.
XX
XX PD 27-JUN-1996.
XX
XX PF 20-DEC-1995; 95WO-AU00868.
XX
XX PR 20-DEC-1994; 94AU-0000157.
XX
XX

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PA (CSLC-) CSL LTD.
PA (UYQU ) UNIV QUEENSLAND.
XX
XX Cox J, Edwards SJ, Frazer I, Webb EA;
XX
XX WPI; 1996-309518/31.
XX
XX N-PSDB; AAT31833.
XX
XX PT Vaccine variants of human papilloma virus antigens - contain
XX variants of E6 and/or E7 protein, pref. deletion mutants, and are
XX used to treat or prevent HPV infection
XX
XX PS Example 1; Page 15-16; 37pp; English.
XX
XX CC A variant of the human papilloma virus (HPV) E6 or E7 protein which
XX elicits a humoral and/or cellular immune response against HPV can be
XX used in vaccines against HPV or to treat HPV infection. The variant
XX is preferably a deletion mutant comprising at least half, and
XX preferably two-thirds of full length E6 or E7 protein starting from
XX the N- or C-terminal, or is a full length E6 moiety fused to a full
XX length E7 moiety. The variant optionally has a linkage moiety and a
XX foreign protein or peptide which facilitates the purification of,
XX and enhances the immunogenicity of, the fusion protein. This
XX sequence is a full length E6/E7 fusion protein.
XX
XX SQ Sequence 266 AA;
XX
XX Query Match 99.1%; Score 843; DB 17; Length 266;
XX Best Local Similarity 99.3%; Pred. No. 1.8e-82;
XX Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCIYVRDGNPY 60
XX |
XX DB 8 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCIYVRDGNPY 67
XX
XX QY 61 AVCDKCLKFYSKYSEYRHYCYSLYGTTLDEQYKKPLCDLLIRINCQKPLCPBEKQRHLD 120
XX |
XX DB 68 AVCDKCLKFYSKYSEYRHYCYSLYGTTLDEQYKKPLCDLLIRINCQKPLCPBEKQRHLD 127
XX
XX QY 121 KQRFNINIRGRTGRCMSCCRSSRTRETQL 151
XX |
XX DB 128 KQRFNINIRGRTGRCMSCCRSSRTRETQL 158
XX
XX RESULT 9
XX AAY25376
XX ID AAY25376 standard; Protein; 273 AA.
XX
XX AC AAY25376;
XX
XX 06-SEP-1999 (first entry)
XX
XX DE HPV fusion protein DI/3-E6-His/HPV16.
XX
XX KW Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
XX immunological fusion partner; CPG oligonucleotide; immune response;
XX HPV antigen; prevention; treatment.
XX
XX OS Synthetic.
XX
XX OS Human papillomavirus.
XX
XX PN WO9933868-A2.
XX
XX PD 08-JUL-1999.
XX
XX PF 18-DEC-1998; 98WO-EP08563.
XX
XX PR 24-DEC-1997; 97GB-0027262.
XX
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX PI Dalemans WLJ, Gerard CMG;
XX
XX

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PF 28-SEP-1993; 93US-0127906.  
 XX  
 PR 30-SEP-1994; 94US-0316239.  
 PR 28-SEP-1993; 93US-0127906.  
 XX  
 PA (UYNE-) UNIV NEW MEXICO STATE.  
 PI Parmenter CA, Wheeler CM;  
 XX WPI: 1997-525714/48.  
 DR N-PSDB; AAT94723.  
 XX  
 PT Evaluating risk of cervical dysplasia or cervical cancer - by  
 PT detecting variant form of human papilloma virus 16  
 XX  
 PS Claim 7; Column 23-24; 33pp; English.  
 CC Methods have been developed for distinguishing a subset of human  
 CC papilloma virus (HPV) that is associated with an increased risk of  
 CC developing cervical dysplasia or cervical cancer. The methods involve:  
 CC (1) preparing a cervical sample to expose any HPV-16 E6 gene in the  
 CC sample and determining if the base at position 350 of the E6 gene  
 CC (see AAT94723 and AAT94724 for comparison) is T or G, where the presence  
 CC of G at position 350 is associated with an increased risk of developing  
 CC cervical dysplasia or cervical cancer; and (2) preparing a cervical  
 CC sample to expose any HPV-16 E6 protein in the sample and determining  
 CC if the amino acid at position 83 of the protein (see position 90 in  
 CC AAW35741 and AAW35742 for comparison) is Val or Leu, where the presence  
 CC of Val at position 83 that is associated with an increased risk of  
 CC developing cervical dysplasia or cervical cancer. The present sequence  
 CC represents the reference protein sequence for HPV-16 E6. The 350G  
 CC variant correlates well with Pap scores: 350T:350G ratios among 45  
 CC HPV16 samples were 10:4 for negative Pap scores; 4:2 for CIN I, 1:6 for  
 CC CIN II; 2:9 for CIN III; 0:3 for cancer.  
 XX  
 SQ Sequence 162 AA:  
 Query Match 99.1%; Score 843; DB 18; Length 162;  
 Best Local Similarity 99.3%; Pred. No. 1e-82;  
 Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MFODPOERPRKLPOLCTELQTTTHDILIECYCKQQLRREYVDFAFRDLCTIYRDGPNY 60  
 DB 8 MFODPOERPRKLPOLCTELQTTTHDILIECYCKQQLRREYVDFAFRDLCTIYRDGPNY 67  
 QY 61 AVCDKCLKEFSKSEYRHYCYSLYGTLLLEQYKPKLDDLIRICINCKPLCPEKORHLD 120  
 DB 68 AVCDKCLKEFSKSEYRHYCYSLYGTLLLEQYKPKLDDLIRICINCKPLCPEKORHLD 127  
 QY 121 KROFHNIRGRWTRGCMSCCRSSRTRETEL 151  
 DB 128 KROFHNIRGRWTRGCMSCCRSSRTRETEL 158  
 RESULT 6  
 AAR63865  
 ID AAR63865 standard; protein; 188 AA.  
 AC AAR63865;  
 XX  
 DT 28-JUN-1995 (first entry)  
 XX  
 DE HPV16 E6/E7 proteins.  
 XX  
 KW HPV16; E6 protein; E7 protein; diagnosis; cervical dysplasia;  
 KW cervix cancer.  
 XX  
 OS Human papillomavirus strain 16.  
 XX  
 FH Key Location/Qualifiers  
 FT Protein 1..158  
 FT /label= E6-protein  
 FT Protein 159..188

FT /label= E7-protein  
 XX  
 PN MO9426934-A.  
 XX  
 PD 24-NOV-1994.  
 XX  
 PF 06-MAY-1994; 94MO-US05085.  
 XX  
 PR 06-MAY-1993; 93US-0058920.  
 XX  
 PA (BAXT ) BAXTER DIAGNOSTICS INC.  
 PI Brown JT;  
 XX WPI: 1995-006821/01.  
 DR P-PSDB; AAO75470.  
 XX  
 PT Human papilloma virus detection assay - by amplification using  
 PT self sustained sequence replication and hybridisation with a  
 PT detector probe  
 XX  
 PS Disclosure; Page 24-26; 79pp; English.  
 XX  
 CC The sequences of the E6 and E7 polypeptide-encoding regions of human  
 CC papillomavirus (HPV) 16 and 18 are given in AAO75470-71 and the  
 CC encoded proteins in AAR63865-66, respectively. Probes and primers  
 CC based on these sequences were used for HPV infection diagnosis;  
 CC expression of E6 and E7 is diagnostic for cervical cancer or pre-  
 CC malignant states.  
 XX  
 SQ Sequence 188 AA:  
 Query Match 99.1%; Score 843; DB 16; Length 188;  
 Best Local Similarity 99.3%; Pred. No. 1.2e-82;  
 Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MFODPOERPRKLPOLCTELQTTTHDILIECYCKQQLRREYVDFAFRDLCTIYRDGPNY 60  
 DB 8 MFODPOERPRKLPOLCTELQTTTHDILIECYCKQQLRREYVDFAFRDLCTIYRDGPNY 67  
 QY 61 AVCDKCLKEFSKSEYRHYCYSLYGTLLLEQYKPKLDDLIRICINCKPLCPEKORHLD 120  
 DB 68 AVCDKCLKEFSKSEYRHYCYSLYGTLLLEQYKPKLDDLIRICINCKPLCPEKORHLD 127  
 QY 121 KROFHNIRGRWTRGCMSCCRSSRTRETEL 151  
 DB 128 KROFHNIRGRWTRGCMSCCRSSRTRETEL 158  
 RESULT 7  
 AAR77725  
 ID AAR77725 standard; protein; 263 AA.  
 AC AAR77725;  
 XX  
 DT 09-MAR-1993 (first entry)  
 XX  
 DE HPV 16 E6 protein fragment.  
 XX  
 KW Virus vector; vaccinia virus; papillomavirus; HPV; human;  
 KW amplification; immunotherapeutic.  
 XX  
 OS Human papillomavirus 16.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..159  
 FT /note= "HPV-16 E6 protein"  
 XX  
 PN WO9216636-A.  
 XX  
 PD 01-OCT-1992.  
 XX  
 PF 10-MAR-1992; 92WO-GB00424.

PI Bernard H, Tan YJ, Beerheide W, Ting AE, Sim MM;  
XX WPI: 2000-256917/22.  
XX  
XX  
XX Polysulfide and dithionodisulfide agents, useful for the treatment or  
XX prophylaxis of diseases caused by mammalian papillomavirus, are  
XX disruptors of a chelated metal cation domain in an MPV gene encoded  
XX protein.  
XX  
XX Disclosure: Fig 1; 78pp; English.  
XX  
XX The present invention describes an agent used in the treatment or  
XX prophylaxis of a disease caused or exacerbated by MPV (mammalian  
XX papillomavirus) comprising a compound capable of reducing, inhibiting  
XX or otherwise decreasing the activity of a protein encoded by an MPV  
XX gene by facilitating disruption of a chelated metal cation domain  
XX present in the protein. An agent of the present invention can be used  
XX to treat cervical cancer or its HPV associated precursor lesions or  
XX other HPV associated cancers and/or warts. The present sequence  
XX represents a human papillomavirus E6 protein containing two zinc  
XX finger motifs, as given in the exemplification of the present  
XX invention.  
XX  
XX Sequence 158 AA;  
SQ  
Query Match 99.1%; Score 843; DB 21; Length 158;  
Best Local Similarity 99.3%; Pred. No. 1e-82;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MFQDPQERPRKLPQCTELQTTIHDIIECVYCKQQLRREYDFAFRLDCTIVYRDGNY 60  
DB 8 MFQDPQERPRKLPQCTELQTTIHDIIECVYCKQQLRREYDFAFRLDCTIVYRDGNY 67  
QY 61 AVCDCCKLFYSKYSERHVCYSLYGTTLEQYKNPKCDLLIRNCINQKPLCEPEKORHD 120  
DB 68 AVCDCCKLFYSKYSERHVCYSLYGTTLEQYKNPKCDLLIRNCINQKPLCEPEKORHD 127  
QY 121 KKQRFHINIRGWTGRMCSGCCRSSRTRRETOL 151  
DB 128 KKQRFHINIRGWTGRMCSGCCRSSRTRRETOL 158  
RESULT 4  
AAB98420  
ID AAB98420 standard; Protein: 158 AA.  
XX  
XX AAB98420;  
XX  
XX 22-AUG-2001 (first entry)  
XX  
XX Human papillomavirus protein HPV16 E6.  
XX  
XX Human papillomavirus; human leukocyte antigen; HLA; immune response;  
XX HPV; epitope; T cell; identification; vaccine; infection; genital wart;  
XX neoplastic growth; antiviral.  
XX  
XX Human papillomavirus.  
XX  
XX WO200141799-A1.  
XX  
XX 14-JUN-2001.  
XX  
XX 11-DEC-2000; 2000WO-US33549.  
XX  
XX 10-DEC-1999; 99US-0172705.  
XX  
XX 15-AUG-2000; 2000US-0641528.  
XX  
XX (EPIIM-) EPIMMUNE INC.  
XX  
XX Sette A, Sidney J, Southwood S, Chesnut R, Celis E, Grey HM;  
XX WPI: 2001-381497/40.  
XX

PI An isolated human papilloma virus (HPV) epitope, useful in vaccines for  
XX treating HPV infections -  
XX  
XX  
XX Disclosure: Page 20-21; 756pp; English.  
XX  
XX The present invention describes an isolated prepared human papillomavirus  
XX (HPV) epitope (1). (1) has antiviral activity, and can be used in  
XX vaccine production. Peptides and corresponding nucleic acid compositions  
XX from the present invention are useful for stimulating an immune response  
XX to HPV by stimulating the production of CTL or HTL responses,  
XX specifically in the treatment or prophylaxis of HPV infection, in persons  
XX who have not manifested symptoms e.g. genital warts or neoplastic growth.  
XX The peptides can also be used in a tetramer staining assay to assess  
XX peripheral blood mononuclear cells for the presence of antigen-specific  
XX CTLs following exposure to a pathogen or immunogen, and as reagents to  
XX evaluate immune recall responses or evaluate the efficacy of a vaccine.  
XX The vaccine compositions are useful for removing warts or treating HPV  
XX infections. The epitopes for inclusion in an epitope-base vaccine may  
XX be selected from conserved regions of viral or tumour-associated  
XX antigens, which reduces the likelihood of escape mutants, also  
XX immunosuppressive epitopes that may be present in whole antigens can be  
XX avoided with the use of epitope-base vaccines. An additional advantage  
XX is the ability to combine selected epitopes (CTL and HTL) and to modify  
XX the composition of the epitopes achieving enhanced immunogenicity, the  
XX major benefit of the vaccine is that is safe and efficacious. AAB98391  
XX to AAB98477 represent polypeptide sequences used in the exemplification  
XX of the present invention.  
XX  
XX Sequence 158 AA;  
SQ  
Query Match 99.1%; Score 843; DB 22; Length 158;  
Best Local Similarity 99.3%; Pred. No. 1e-82;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MFQDPQERPRKLPQCTELQTTIHDIIECVYCKQQLRREYDFAFRLDCTIVYRDGNY 60  
DB 8 MFQDPQERPRKLPQCTELQTTIHDIIECVYCKQQLRREYDFAFRLDCTIVYRDGNY 67  
QY 61 AVCDCCKLFYSKYSERHVCYSLYGTTLEQYKNPKCDLLIRNCINQKPLCEPEKORHD 120  
DB 68 AVCDCCKLFYSKYSERHVCYSLYGTTLEQYKNPKCDLLIRNCINQKPLCEPEKORHD 127  
QY 121 KKQRFHINIRGWTGRMCSGCCRSSRTRRETOL 151  
DB 128 KKQRFHINIRGWTGRMCSGCCRSSRTRRETOL 158  
RESULT 5  
AAW35741  
ID AAW35741 standard; Protein: 162 AA.  
XX  
XX AAW35741;  
XX  
XX 16-FEB-1998 (first entry)  
XX  
XX Human papillomavirus type 16 E6 protein.  
XX  
XX Complete genome; circular; human papillomavirus type 16; HPV16 E6;  
XX cervical dysplasia; cervical cancer; cervical smear.  
XX  
XX Human papillomavirus type 16.  
XX  
XX  
XX Key Location/Qualifiers  
XX  
XX Misc-difference 90  
XX FT /note= "Mutated to Val in the variant"  
XX FT Misc-difference 159  
XX FT /note= "End of protein sequence even though 3 amino  
XX FT acid residues are given following on"  
XX  
XX US5679509-A.  
XX  
XX 21-OCT-1997.  
XX

XX Example 2: Fig 9; 73pp; English.

PS The present invention describes a polypeptide comprising a  
CC transcriptional adaptor motif (TRAM) or a TRAM-interaction motif  
CC (TRIM) (I). (I) can be used for identifying compounds (II) comprising a  
CC polypeptide capable of disrupting an interaction between a TRAM sequence  
CC and/or a TRIM sequence. Polypeptides which bind to a TRAM sequence or a  
CC TRIM sequence are identified by incubating, the polypeptide with (I) and  
CC determining if the polypeptide interacts with (I). Compound (II) is  
CC useful for preparing a pharmaceutical composition and for disrupting an  
CC interaction between TRAM sequence and TRIM sequence in vitro, thereby  
CC inhibiting viral transcription or cell cycle progression in mammalian  
CC cells especially cancer cell. Compounds which disrupt interaction  
CC between TRIM/TRAM containing polypeptides can be used therapeutically to  
CC prevent or treat viral diseases and tumours. The polypeptides reduce  
CC susceptibility of cells to viral infection and regulate cell cycle  
CC including apoptosis and growth arrest and can be used to produce  
CC antibodies against the TRIM or TRAM sequences. HPV types associated  
CC with high risk or low risk of cervical cancer can be distinguished  
CC based on the ability of E6 polypeptides to bind to creb binding protein  
CC (CBP) TRAM sequence. The present sequence represents a HPV-16 E6 protein  
CC amino acid sequence from an example from the present invention.

XX Sequence 151 AA:

Query Match 100.0%; Score 851; DB 21; Length 151;  
Best Local Similarity 100.0%; Pred. No. 1.3e-83;  
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPQCTELQTTIHDIIECYCKQQLRREVDFAFRDLCIYRDGNPY 60  
DB 1 MFODPQERPRKLPQCTELQTTIHDIIECYCKQQLRREVDFAFRDLCIYRDGNPY 60  
QY 61 AVCDKCLKFSKYSEYRHYCYSLXGTLLEQYKPLCDLLIRINCQKPLCPBEKQRLHD 120  
DB 61 AVCDKCLKFSKYSEYRHYCYSLXGTLLEQYKPLCDLLIRINCQKPLCPBEKQRLHD 120  
QY 121 KQRFNHRGWRMTGRSCSCSSRTRETOL 151  
DB 121 KQRFNHRGWRMTGRSCSCSSRTRETOL 151

RESULT 2  
AAR22766  
ID AAR22766 standard; peptide; 158 AA.

XX AAR22766;  
AC 21-SEP-1992 (first entry)  
DT 21-SEP-1992 (first entry)  
XX HPV E6 peptide.  
DE  
XX Human; papillomavirus; immunogenic; cervical; warts; carcinoma;  
KW cancer.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN W09205248-A.  
XX  
PD 02-APR-1992.  
XX  
PF 26-SEP-1991; 91WO-US07081.  
XX  
PR 26-SEP-1990; 90US-0588384.  
XX  
PA (BRIM ) BRISTOL-MYERS SQUIB.  
XX  
PI Blake J, Chen L, Hellstrom I, Hellstrom K, Hu S L;  
XX Thomas E K;  
XX  
DR WPI; 1992-132119/16.

XX Immunogenic peptide(s) derived from E6 or E7 region of HPV16 -  
PT and recombinant cells encoding them, useful in treatment and  
PT prophylaxis of cervical warts or cancer resulting from HPV  
PT infection  
PS Disclosure; Fig 7; 81pp; English.

CC The peptide is the sequence of the human papillomavirus HPV 16 E6  
CC nucleoprotein. Peptides corresponding to regions (pref. epitopic  
CC regions) of HPV 16 E6 were synthesised by standard Merrifield  
CC syntheses. Examples of such peptides are E6 1-20, 8-20, 119-134 or  
CC 148-158. Compositions contg. these peptides, antibodies against the  
CC peptides, or recombinant cells contg. the gene encoding the immuno-  
CC genic peptides may be utilised in methods for inhibiting and treating  
CC HPV infection and tumour initiation and progression e.g. in the  
CC prevention or retardation of cervical warts and cervical carcinoma  
CC resulting from HPV infection.  
CC See also AAR22767.

XX Sequence 158 AA:

Query Match 99.1%; Score 843; DB 13; Length 158;  
Best Local Similarity 99.3%; Pred. No. 1e-82;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPQCTELQTTIHDIIECYCKQQLRREVDFAFRDLCIYRDGNPY 60  
DB 8 MFODPQERPRKLPQCTELQTTIHDIIECYCKQQLRREVDFAFRDLCIYRDGNPY 67  
QY 61 AVCDKCLKFSKYSEYRHYCYSLXGTLLEQYKPLCDLLIRINCQKPLCPBEKQRLHD 120  
DB 68 AVCDKCLKFSKYSEYRHYCYSLXGTLLEQYKPLCDLLIRINCQKPLCPBEKQRLHD 127  
QY 121 KQRFNHRGWRMTGRSCSCSSRTRETOL 151  
DB 128 KQRFNHRGWRMTGRSCSCSSRTRETOL 158

RESULT 3  
AAV82462  
ID AAV82462 standard; Protein; 158 AA.

XX AAV82462;  
AC 30-JUN-2000 (first entry)  
DT  
XX Human papillomavirus E6 protein containing two zinc finger motifs.  
DE  
XX Chelated zinc finger; therapeutic; treatment; prophylaxis; HPV;  
KW mammalian papillomavirus; antiviral; cytostatic; cervical cancer;  
KW lesion; wart.  
XX  
OS Human papillomavirus.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 37..73  
FT /note="forms a zinc finger motif"  
FT Misc-difference 110..146  
FT /note="forms a zinc finger motif"  
XX  
PN W0200014063-A1.  
XX  
PD 16-MAR-2000.  
XX  
PF 03-SEP-1999; 99WO-AU00724.  
XX  
PR 04-SEP-1998; 98AU-0005733.  
PR 15-JUL-1999; 99AU-0001645.  
XX  
PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.  
PA (HUGH/) HUGHES E J L.  
XX

GenCore Version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 13, 2002, 08:31:04 : Search time 58.362 Seconds  
(without alignments)  
344.760 Million cell updates/sec

Title: US-09-701-080c-18  
Perfect score: 851  
Sequence: 1 MFQDPEPRPKLPOLCTEHLQ.....WTGRCMSCCRSSRTREPOL 151

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 13350620 residues  
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	851	100.0	151	21	AAV57808
2	843	99.1	158	13	AAK22766
3	843	99.1	158	21	AAV82462
4	843	99.1	158	22	AAV8420
5	843	99.1	162	18	AAV35741
6	843	99.1	188	16	AAV63855
7	843	99.1	263	13	AAK27725
8	843	99.1	266	17	AAV97561
9	843	99.1	273	20	AAV25376
10	843	99.1	273	20	AAV02632

11	843	99.1	292	20	AAV25379	HPV fusion protein
12	843	99.1	292	20	AAV02635	CLYRA-E6-His prote
13	843	99.1	371	20	AAV25377	HPV fusion protein
14	843	99.1	371	20	AAV02633	Prot.DI/3-E6-E7-H1
15	843	99.1	330	20	AAV25381	HPV fusion protein
16	843	99.1	330	20	AAV02637	CLYRA-E6E7-His pro
17	840	98.7	162	18	AAV35742	Human papillomavir
18	799.5	93.9	243	20	AAV93659	Papillomavirus E6/
19	594	69.8	149	14	AAV40919	HPV E6 region prod
20	538	63.2	149	22	AAV98444	Human papillomavir
21	534	62.7	149	22	AAV98447	Human papillomavir
22	487	57.2	172	17	AAV97563	Human papilloma v1
23	477	56.1	172	17	AAV97562	Human papilloma v1
24	469.5	55.2	158	16	AAV96566	HPV-18 E6 protein.
25	469.5	55.2	158	16	AAV63866	HPV18 E6/E7 protel
26	469.5	55.2	158	20	AAV39968	HPV-18 E6 protein
27	469.5	55.2	158	21	AAV03176	HPV-18 E6 protein.
28	469.5	55.2	158	22	AAV98427	Human papillomavir
29	469.5	55.2	271	13	AAV27728	HPV fusion protein
30	469.5	55.2	278	20	AAV25385	Prot.DI/3-E6-His/H
31	469.5	55.2	278	20	AAV02641	HPV fusion protein
32	469.5	55.2	383	20	AAV25386	Prot.DI/3-E6-E7-H1
33	469.5	55.2	383	20	AAV02642	Human papillomavir
34	460.5	54.1	158	22	AAV98440	Human papillomavir
35	441.5	51.9	155	22	AAV98452	Human papillomavir
36	332	38.9	236	22	AAV96052	Polyepitope polype
37	331	39.0	117	22	AAV96050	Polyepitope polype
38	321	37.7	150	22	AAV98395	Human papillomavir
39	320	37.6	150	22	AAV98404	Human papillomavir
40	320	37.6	368	18	AAV01808	Human papillomavir
41	320	37.6	375	18	AAV01809	Human papillomavir
42	320	37.6	465	18	AAV01810	Human papillomavir
43	320	37.6	1587	18	AAV01815	Human papillomavir
44	310	36.4	150	22	AAV98413	Human papillomavir
45	197	23.1	119	22	AAV96051	Polyepitope polype

ALIGNMENTS

RESULT 1  
AAV57808  
ID AAV57808 standard; peptide: 151 AA.  
XX  
AC AAV57808;  
DT 20-MAR-2000 (first entry).  
XX  
DE HPV-16 E6 protein amino acid sequence.  
XX  
KW Transcriptional adapter motif; TRAM, TRAM interaction motif; TRIM.  
KW creb binding protein; transcriptional regulation; cytosolic; antiviral;  
KW cell cycle inhibitor; viral transcription inhibitor; cancer; tumour;  
KW viral disease; viral infection; cell cycle; apoptosis; growth arrest.  
XX  
OS Human papillomavirus.  
XX  
PN WO961608-A2.  
XX  
PD 02-DEC-1999.  
XX  
PE 26-MAY-1999; 99MO-GH01668.  
XX  
PR 26-MAY-1998; 98GB-0011303.  
PR 05-JAN-1999; 99GB-0000157.  
PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.  
XX  
PI O'Connor MJ, Zimmermann H;  
XX  
DR WPI; 2000-072620/06.  
XX  
PT Novel polypeptides cells useful for treating viral disease and cancer

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 13, 2002, 08:38:45 ; Search time 24.0859 Seconds  
(without alignments)  
420.734 Million cell updates/sec

Title: US-09-701-080C-18

Perfect score: 851

Sequence: 1 MFQDPERPRKLPOLCTELQ.....WTGRMCCRSRRTRRETQL 151

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 239201 seqs, 67110966 residues

Total number of hits satisfying chosen parameters: 239201

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Post-Processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	851	100.0	151	5	US-09-701-080C-18
2	843	99.1	273	5	US-09-581-976B-4
3	843	99.1	292	5	US-09-581-976B-10
4	843	99.1	371	5	US-09-581-976B-6
5	843	99.1	390	5	US-09-581-976B-14
6	833	97.9	151	6	US-10-177-390-6
7	469.5	55.2	278	5	US-09-581-976B-21
8	469.5	55.2	383	5	US-09-581-976B-23
9	90.5	10.6	572	6	US-10-240-851-107
10	85	10.0	479	5	US-09-724-676-54539
11	85	10.0	479	5	US-09-724-676-54540
12	85	10.0	479	5	US-09-724-676-54541
13	85	10.0	479	5	US-09-724-676-54542
14	85	10.0	479	5	US-09-724-676-54543
15	85	10.0	479	5	US-09-724-676-54544
16	85	10.0	479	5	US-09-724-676-54545
17	85	10.0	479	5	US-09-724-676-54546
18	85	10.0	479	5	US-09-724-676-54547
19	85	10.0	479	5	US-09-724-676-54548
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23	85	10.0	479	5	US-09-724-676-54552
24	85	10.0	479	5	US-09-724-676-54553
25	85	10.0	479	5	US-09-724-676-54554
26	85	10.0	479	5	US-09-724-676-54555

27	85	10.0	479	5	US-09-724-676A-54547	Sequence 54547, A
28	85	10.0	513	5	US-09-724-676-54554	Sequence 54554, A
29	85	10.0	513	5	US-09-724-676-54555	Sequence 54555, A
30	85	10.0	513	5	US-09-724-676-54556	Sequence 54556, A
31	85	10.0	513	5	US-09-724-676-54557	Sequence 54557, A
32	85	10.0	513	5	US-09-724-676-54558	Sequence 54558, A
33	85	10.0	513	5	US-09-724-676-54559	Sequence 54559, A
34	85	10.0	513	5	US-09-724-676-54560	Sequence 54560, A
35	85	10.0	513	5	US-09-724-676-54561	Sequence 54561, A
36	85	10.0	513	5	US-09-724-676-54562	Sequence 54562, A
37	85	10.0	513	5	US-09-724-676A-54554	Sequence 54554, A
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40	85	10.0	513	5	US-09-724-676A-54557	Sequence 54557, A
41	85	10.0	513	5	US-09-724-676A-54558	Sequence 54558, A
42	85	10.0	513	5	US-09-724-676A-54559	Sequence 54559, A
43	85	10.0	513	5	US-09-724-676A-54560	Sequence 54560, A
44	85	10.0	513	5	US-09-724-676A-54561	Sequence 54561, A
45	85	10.0	513	5	US-09-724-676A-54562	Sequence 54562, A

## ALIGNMENTS

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RESULT 1
US-09-701-080C-18
; Sequence 18, Application US/09701080C
; GENERAL INFORMATION:
; APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY
; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P30
; FILE REFERENCE: N73477C GCM
; CURRENT APPLICATION NUMBER: US/09/701,080C
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: GB 9811303.8
; PRIOR FILING DATE: 1998-05-26
; PRIOR APPLICATION NUMBER: GB 9900157.0
; PRIOR FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-09-701-080C-18

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Best Local Similarity 100.0%; Pred. No. 2.6e-84;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      61 AVDCDKLTKYKSEYRHYCYSLYGTLLRQYKPLCDLLIRINCOKPLCEKORHDD 120
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QY      61 AVDCDKLTKYKSEYRHYCYSLYGTLLRQYKPLCDLLIRINCOKPLCEKORHDD 120
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DB      61 AVDCDKLTKYKSEYRHYCYSLYGTLLRQYKPLCDLLIRINCOKPLCEKORHDD 120
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QY      121 KQRFNINRGWTRGMSCCRSRRTRRETQL 151
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DB      121 KQRFNINRGWTRGMSCCRSRRTRRETQL 151
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RESULT 2
US-09-581-976B-4
; Sequence 4, Application US/09581976B
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/09/581,976B
; CURRENT FILING DATE: 2000-06-20

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? PRIOR FILING DATE: 1998-12-18
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? PRIOR FILING DATE: 1997-12-24
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?
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?
? TYPE: PRT
?
? ORGANISM: Artificial Sequence
?
? FEATURE:
?
? OTHER INFORMATION: Chimaeic protein (protein D from Haemophilus
? OTHER INFORMATION: Influenza B and E6 from Human papilloma virus type
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Matches 150;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0

Qy	1	MEODPEERPRLLPOLCETELQTTIDHILLECVCCKQOLLREVDYFAFADICLCIYRDSNPY	60
Db	114	MEODPEERPRLLPOLCETELQTTIDHILLECVCCKQOLLREVDYFAFADICLCIYRDSNPY	173
Qy	61	AVCCKCLKEFVSEAEYRHVYCYSLGTLLLEOYNKPRCDLLIRCTNCKRPLCPBEKONHL	120
Db	174	AVCCKCLKEFVSEAEYRHVYCYSLGTLLLEOYNKPRCDLLIRCTNCKRPLCPBEKONHL	233
Qy	121	KKQRFHNIRGWTGRCMSCCSSRTRETL	151
Db	234	KKQRFHNIRGWTGRCMSCCSSRTRETL	264

RESULT 3  
ITS-09-58

```

Sequence 10, Application US/09581976B
GENERAL INFORMATION:
APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Geraud, Catherine Marie Ghislaine
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/09/581,976B
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 292
TYPE: PRN
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chimaeric protein (Clyta from Streptococcus
OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus
OTHER INFORMATION: 16)
US-09-581-976B-10

```

```

Query Match      99.1%   Score 843;   DB 5;   Length 292;
Best Local Similarity 99.3%   Pred. No. 3.6e-83;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0

```

QY	1	MFQOPQRPRLPOLCJLELQTTIIDILIECYVCKQOQLKREBYVDFADRLDLCIYRQBNPY	60
QY			
Db	133	MFQOPQRPRLPOLCJLELQTTIIDILIECYVCKQOQLKREBYVDFADRLDLCIYRQBNPY	1922
QY	61	AVCDCKLKFYSKYSEYRHYCYSLYGTTLLEOQYNKPLCDLIRINCQKPLCPBEKORHLD	120
QY			
Db	193	AVCDCKLKFYSKYSEYRHYCYSLYGTTLLEOQYNKPLCDLIRINCQKPLCPBEKORHLD	2522
QY	121	KKQRFHNIIRGHWIGRCHSCCRSSXTRETFOL	151
QY			

Db 253 KQRFHNIRGWTGRCMSCCRSSRTRETQL 283

RESULT 4  
HS-09-581-976B-6

```

Sequence 6, Application US/095811976B
GENERAL INFORMATION:
APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/09/581,976B
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/PP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 371
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: ChimERIC protein (protein D from Haemophilus
OTHER INFORMATION: Influenza B and E6E7 fusion from Human papilloma
OTHER INFORMATION: virus type 16)
IS-09-581-976B-

```

Query Match	99.1%	Score 843;	DB 5;	Length 371;
Best Local Similarity	99.3%	Pred. NO. 4.5e-83;		
Matches 150; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	1	MFQDQBERPRKLPOLCSTELQTTIHDIILLECVCYCKQQLIREVYDFAERDLCIYRGQNPY	60
Db	114	MFQDQBERPRKLPOLCSTELQTTIHDIILLECVCYCKQQLIREVYDFAERDLCIYRGQNPY	173
QY	61	AVCDCKLKFYSKYSEYHNYCYSLYGTTLEOYNKPLCDDLRCINCKPLCPREKORHLD	120
Db	174	AVCDCKLKFYSKYSEYHNYCYSLYGTTLEOYNKPLCDDLRCINCKPLCPREKORHLD	233
QY	121	KKQRFHNRIGHWGRCMSSCCSSRTRETDL	151
Db	234	KKQRFHNRIGHWGRCMSSCCSSRTRETDL	264

RESULT 5  
US-09-581-976B-14

```

1  APPLICANT: Dalemans Wilfried L.J.
2  APPLICANT: Gerard, Catherine Marie Ghislaine
3  TITLE OF INVENTION: Vaccine
4  FILE REFERENCE: BA5124
5  CURRENT APPLICATION NUMBER: US/09/581,976B
6  PRIOR FILING DATE: 2000-06-20
7  PRIOR APPLICATION NUMBER: PCT/EP98/08563
8  PRIOR FILING DATE: 1998-12-18
9  PRIOR APPLICATION NUMBER: GB 9727262.9
10 PRIOR FILING DATE: 1997-12-24
11 NUMBER OF SEQ. ID NOS: 28
12 SOFTWARE: FastSeq for Windows Version 3.0
13 SEQ. ID NO 14
14 LENGTH: 390

```

```

; ORGANISM: Artificial Sequence
;
; FEATURE:
;
; OTHER INFORMATION: Chimeric protein (Clyta from Streptococcus
;
; OTHER INFORMATION: pneumoniae and E6E7 fusion from Human papillomaoma
;
; OTHER INFORMATION: virus type 16)
;
; OS-09-581-976B-14

```

query match 99.18; Score 843; DB 5; Length 390;

Best Local Similarity 99.3%; Pred. No. 4.7e-83;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFOODPERPRKLPOLCTELQTTIHDIIEECVYCKOOLLREYVDFAFRDLCTIVYRDGNPY 60  
|||  
DB 133 MFOODPERPRKLPOLCTELQTTIHDIIEECVYCKOOLLREYVDFAFRDLCTIVYRDGNPY 192  
QY 61 AVCDKCLFKFSKYSEYRHYCSLYGTTLEQOYNKPLCDLLIRINCINOKPLCEPEKORHLD 120  
|||  
DB 193 AVCDKCLFKFSKYSEYRHYCSLYGTTLEQOYNKPLCDLLIRINCINOKPLCEPEKORHLD 252  
QY 121 KQRFHNINGRMTGRCMSSCRSSRTRETOL 151  
|||  
DB 253 KQRFHNINGRMTGRCMSSCRSSRTRETOL 283

RESULT 6  
US-10-177-390-6  
; Sequence 6, Application US/10177390  
; GENERAL INFORMATION:  
; APPLICANT: Schuier, Gerold  
; APPLICANT: N.V. Antwerp Innovatiecentrum  
; TITLE OF INVENTION: Improved transfection of Eucaryotic Cells with linear  
; FILE REFERENCE: 021505wo/3H/ml  
; CURRENT APPLICATION NUMBER: US/10/177,390  
; CURRENT FILING DATE: 2002-06-20  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentl Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 151  
; TYPE: PRP  
; ORGANISM: Human papillomavirus type 16  
US-10-177-390-6

Query Match 97.9%; Score 833; DB 6; Length 151;  
Best Local Similarity 98.0%; Pred. No. 2.3e-82;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFOODPERPRKLPOLCTELQTTIHDIIEECVYCKOOLLREYVDFAFRDLCTIVYRDGNPY 60  
|||  
DB 1 MFOODPERPRKLPOLCTELQTTIHDIIEECVYCKOOLLREYVDFAFRDLCTIVYRDGNPY 60  
QY 61 AVCDKCLFKFSKYSEYRHYCSLYGTTLEQOYNKPLCDLLIRINCINOKPLCEPEKORHLD 120  
|||  
DB 61 AVCDKCLFKFSKYSEYRHYCSLYGTTLEQOYNKPLCDLLIRINCINOKPLCEPEKORHLD 120  
QY 121 KQRFHNINGRMTGRCMSSCRSSRTRETOL 151  
|||  
DB 121 KQRFHNINGRMTGRCMSSCRSSRTRETOL 151

RESULT 7  
US-09-581-976B-21  
; Sequence 21, Application US/09581976B  
; GENERAL INFORMATION:  
; APPLICANT: Dalemans, Wilfried L.J.  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45124  
; CURRENT APPLICATION NUMBER: US/09/581,976B  
; CURRENT FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: PCT/EP98/08563  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: GB 9727262.9  
; PRIOR FILING DATE: 1997-12-24  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 21  
; LENGTH: 278  
; TYPE: PRP  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Chimeric protein (protein D from Haemophilus  
; OTHER INFORMATION: Influenza B and E6 from Human papilloma virus type  
; OTHER INFORMATION: 18)  
US-09-581-976B-21

Query Match 55.2%; Score 469.5; DB 5; Length 278;  
Best Local Similarity 56.1%; Pred. No. 5.2e-43;  
Matches 87; Conservative 22; Mismatches 41; Indels 5; Gaps 1;

QY 2 FODPOERPRKLPOLCTELQTTIHDIIEECVYCKOOLLREYVDFAFRDLCTIVYRDGNPY 61  
|||  
DB 115 FODPOERPRKLPOLCTELQTTIHDIIEECVYCKOOLLREYVDFAFRDLCTIVYRDGNPY 174  
QY 62 VCDKCLFKFSKYSEYRHYCSLYGTTLEQOYNKPLCDLLIRINCINOKPLCEPEKORHLD 121  
|||  
DB 175 VCDKCLFKFSKYSEYRHYCSLYGTTLEQOYNKPLCDLLIRINCINOKPLCEPEKORHLD 234  
QY 122 KQRFHNINGRMTGRCMSSCRSSRTRETOL 151  
|||  
DB 235 KQRFHNINGRMTGRCMSSCRSSRTRETOL 269

RESULT 8  
US-09-581-976B-23  
; Sequence 23, Application US/09581976B  
; GENERAL INFORMATION:  
; APPLICANT: Dalemans, Wilfried L.J.  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45124  
; CURRENT APPLICATION NUMBER: US/09/581,976B  
; CURRENT FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: PCT/EP98/08563  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: GB 9727262.9  
; PRIOR FILING DATE: 1997-12-24  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 23  
; LENGTH: 383  
; TYPE: PRP  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chimeric protein (protein D from Haemophilus  
; OTHER INFORMATION: Influenza B and E6E7 fusion from Human papilloma  
; OTHER INFORMATION: virus type 18)  
US-09-581-976B-23

Query Match 55.2%; Score 469.5; DB 5; Length 383;  
Best Local Similarity 56.1%; Pred. No. 7.1e-43;  
Matches 87; Conservative 22; Mismatches 41; Indels 5; Gaps 1;

QY 2 FODPOERPRKLPOLCTELQTTIHDIIEECVYCKOOLLREYVDFAFRDLCTIVYRDGNPY 61  
|||  
DB 115 FODPOERPRKLPOLCTELQTTIHDIIEECVYCKOOLLREYVDFAFRDLCTIVYRDGNPY 174  
QY 62 VCDKCLFKFSKYSEYRHYCSLYGTTLEQOYNKPLCDLLIRINCINOKPLCEPEKORHLD 121  
|||  
DB 175 VCDKCLFKFSKYSEYRHYCSLYGTTLEQOYNKPLCDLLIRINCINOKPLCEPEKORHLD 234  
QY 122 KQRFHNINGRMTGRCMSSCRSSRTRETOL 151  
|||  
DB 235 KQRFHNINGRMTGRCMSSCRSSRTRETOL 269

RESULT 9  
US-10-240-851-107  
; Sequence 107, Application US/10240851  
; GENERAL INFORMATION:  
; APPLICANT: John P. Carulli et al.  
; TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3  
; FILE REFERENCE: 032796-021  
; CURRENT APPLICATION NUMBER: US/10/240,851

```
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US 09/544,398
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/543,771
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 109
; SEQ ID NO 107
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-240-851-107
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```
Query Match 10.6%; Score 90.5; DB 6; Length 572;
Best Local Similarity 23.5%; Pred. No. 0.062;
Matches 43; Conservative 20; Mismatches 65; Indels 55; Gaps 11;
```

```
OY 1 MFQD---PQRPRKLPQLC-----TELOTTHDIIIECVYCKQOLLREYV 43
DB 366 LMDMEHPQONVAVNELGCRHQPLARAQPAVARALGQLFIACFTCHQCAQOLGQOFC 425
OY 44 DFAFRDLCI-VYRD-----GNPYAVCDKLFYKSEYRHYCS-----LYGTT 87
DB 426 SLEGAPRCGECYDTLEKCTGCEP---ITRMLRATCK--AHPHCTCYVVCARPLEGTS 481
OY 88 -LEQYKPKLC-----DLLIRICINCKPLCPE---EKORHLDKKQRFHNRGRTGRC 136
DB 482 FIYDQANRPHCPVDYHKKQYAPRCVSCSEPIPEGRDETVRVVALDKNFHM-----KC 534
OY 137 MSC 139
DB 535 YKC 537
```

```
RESULT 10
US-09-724-676-54539
; Sequence 54539, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54539
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-54539
```

```
Query Match 10.0%; Score 85; DB 5; Length 479;
Best Local Similarity 19.9%; Pred. No. 0.2;
Matches 30; Conservative 22; Mismatches 41; Indels 58; Gaps 7;
```

```
OY 14 QLCLEQTTHDIIIECVYCKQOLLREYVDFAFRDLCTIYRDGNPYAVCDKLFYKSKY 73
DB 334 QVVTAMGKTWHPHEVCTHGOEIGSRNFE-----RDGQPY--CEK--DYHNLF 379
OY 74 SEYRHYCYSLYGTTLLEQYKPKPLCDLLIR-----CINCKPLCPREEKQRHLDK 121
DB 380 SPRCYVC-----NGPILDKVVYVALDRTWHPHEFCAQCGAFGPE----- 419
OY 122 KORFHNIRGR-----WTGRMSSCCRS 142
DB 420 --GFHEKDGKAYCRKDYFDMFAPKCGGCARA 448
```

```
RESULT 11
US-09-724-676-54540
; Sequence 54540, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54540
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-54540
```

```
Query Match 10.0%; Score 85; DB 5; Length 479;
Best Local Similarity 19.9%; Pred. No. 0.2;
Matches 30; Conservative 22; Mismatches 41; Indels 58; Gaps 7;
```

```
OY 14 QLCLEQTTHDIIIECVYCKQOLLREYVDFAFRDLCTIYRDGNPYAVCDKLFYKSKY 73
DB 334 QVVTAMGKTWHPHEVCTHGOEIGSRNFE-----RDGQPY--CEK--DYHNLF 379
OY 74 SEYRHYCYSLYGTTLLEQYKPKPLCDLLIR-----CINCKPLCPREEKQRHLDK 121
DB 380 SPRCYVC-----NGPILDKVVYVALDRTWHPHEFCAQCGAFGPE----- 419
OY 122 KORFHNIRGR-----WTGRMSSCCRS 142
DB 420 --GFHEKDGKAYCRKDYFDMFAPKCGGCARA 448
```

```
RESULT 12
US-09-724-676-54541
; Sequence 54541, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54541
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-54541
```

```
Query Match 10.0%; Score 85; DB 5; Length 479;
Best Local Similarity 19.9%; Pred. No. 0.2;
Matches 30; Conservative 22; Mismatches 41; Indels 58; Gaps 7;
```

```
OY 14 QLCLEQTTHDIIIECVYCKQOLLREYVDFAFRDLCTIYRDGNPYAVCDKLFYKSKY 73
DB 334 QVVTAMGKTWHPHEVCTHGOEIGSRNFE-----RDGQPY--CEK--DYHNLF 379
OY 74 SEYRHYCYSLYGTTLLEQYKPKPLCDLLIR-----CINCKPLCPREEKQRHLDK 121
DB 380 SPRCYVC-----NGPILDKVVYVALDRTWHPHEFCAQCGAFGPE----- 419
OY 122 KORFHNIRGR-----WTGRMSSCCRS 142
DB 420 --GFHEKDGKAYCRKDYFDMFAPKCGGCARA 448
```

```
RESULT 13
US-09-724-676-54542
; Sequence 54542, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
```



```
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54542
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-54542

Query Match
Best Local Similarity 19.9%; Score 85; DB 5; Length 479;
Matches 30; Conservative 22; Mismatches 41; Indels 58; Gaps 7;

QY 14 QCTELQTTIHDIIECYCKQQLRREYDFAFRDLCTIVYRDGNPYAVCDKCLFYSKY 73
DB 334 QVVTAMGKTWHEHVCYTHCQEEIGSRNFFE-----RDGQPY--CEK--DYHNL 379
QY 74 SEYRHVCSLYGTLEEQYNKPLCDLLR-----CINQKPLCPPEKQRHLDK 121
DB 380 SPRCYC-----NSPILDKVYVALDRTWHPHFCAQCGAFGPE----- 419
QY 122 KORFNINGR-----WTGRCSGCCRS 142
DB 420 --GFHEKDGKAYCRKDYFDMFAPKCGGCARA 448

RESULT 14
US-09-724-676-54543
; Sequence 54543, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54543
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-54543

Query Match
Best Local Similarity 19.9%; Score 85; DB 5; Length 479;
Matches 30; Conservative 22; Mismatches 41; Indels 58; Gaps 7;

QY 14 QCTELQTTIHDIIECYCKQQLRREYDFAFRDLCTIVYRDGNPYAVCDKCLFYSKY 73
DB 334 QVVTAMGKTWHEHVCYTHCQEEIGSRNFFE-----RDGQPY--CEK--DYHNL 379
QY 74 SEYRHVCSLYGTLEEQYNKPLCDLLR-----CINQKPLCPPEKQRHLDK 121
DB 380 SPRCYC-----NSPILDKVYVALDRTWHPHFCAQCGAFGPE----- 419
QY 122 KORFNINGR-----WTGRCSGCCRS 142
DB 420 --GFHEKDGKAYCRKDYFDMFAPKCGGCARA 448

RESULT 15
US-09-724-676-54544
; Sequence 54544, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
```

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54544
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-54544
```

```
Query Match
Best Local Similarity 19.9%; Score 85; DB 5; Length 479;
Matches 30; Conservative 22; Mismatches 41; Indels 58; Gaps 7;

QY 14 QCTELQTTIHDIIECYCKQQLRREYDFAFRDLCTIVYRDGNPYAVCDKCLFYSKY 73
DB 334 QVVTAMGKTWHEHVCYTHCQEEIGSRNFFE-----RDGQPY--CEK--DYHNL 379
QY 74 SEYRHVCSLYGTLEEQYNKPLCDLLR-----CINQKPLCPPEKQRHLDK 121
DB 380 SPRCYC-----NSPILDKVYVALDRTWHPHFCAQCGAFGPE----- 419
QY 122 KORFNINGR-----WTGRCSGCCRS 142
DB 420 --GFHEKDGKAYCRKDYFDMFAPKCGGCARA 448
```

Search completed: December 13, 2002, 08:45:52  
Job time : 25.0859 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 13, 2002, 08:37:10 : Search time 252.902 Seconds  
(without alignments)  
384.951 Million cell updates/sec

Title: US-09-701-080C-18

Perfect score: 851

Sequence: 1 MFQDPERRKLPQLCTELQ.....WTGRCSGCRSSRRRTRETQL 151

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Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

4569144

Total number of hits satisfying chosen parameters:

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_AA\_Main:\*

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2: /cgn2\_6/ptodata/1/paa/US06.COMB.pep:\*  
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13: /cgn2\_6/ptodata/1/paa/US089.COMB.pep:\*  
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23: /cgn2\_6/ptodata/1/paa/US099.COMB.pep:\*  
24: /cgn2\_6/ptodata/1/paa/US100.COMB.pep:\*  
25: /cgn2\_6/ptodata/1/paa/US101.COMB.pep:\*  
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27: /cgn2\_6/ptodata/1/paa/US60.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	851	100.0	151	21	US-09-701-080A-18
2	843	99.1	158	1	PCT-US00-33549-31
3	843	99.1	158	23	US-09-980-523A-2
4	843	99.1	273	19	US-09-581-976-4
5	843	99.1	273	24	US-10-000-903-4
6	843	99.1	292	19	US-09-581-976-10

7	843	99.1	292	24	US-10-000-903-10	Sequence 10, Appl
8	843	99.1	371	19	US-09-581-976-6	Sequence 6, Appl
9	843	99.1	371	24	US-10-000-903-6	Sequence 6, Appl
10	843	99.1	390	19	US-09-581-976-14	Sequence 14, Appl
11	843	99.1	390	24	US-10-000-903-14	Sequence 14, Appl
12	840	98.7	151	27	US-60-306-809-20	Sequence 20, Appl
13	840	98.7	151	27	US-60-415-929-13	Sequence 13, Appl
14	840	98.7	248	27	US-60-415-929-13	Sequence 1, Appl
15	835	98.1	248	27	US-60-415-929-7	Sequence 7, Appl
16	833	97.9	151	15	US-09-177-390-6	Sequence 6, Appl
17	816	95.9	248	27	US-60-415-929-3	Sequence 3, Appl
18	816	95.9	248	27	US-60-415-929-5	Sequence 5, Appl
19	811	95.3	248	27	US-60-415-929-9	Sequence 9, Appl
20	811	95.3	248	27	US-60-415-929-11	Sequence 11, Appl
21	799.5	93.9	243	18	US-09-462-993-1	Sequence 1, Appl
22	538	63.2	149	1	PCT-US00-33549-45	Sequence 45, Appl
23	534	62.7	149	1	PCT-US00-33549-58	Sequence 58, Appl
24	469.5	55.2	158	1	PCT-US00-33549-38	Sequence 38, Appl
25	469.5	55.2	158	5	US-08-176-937A-4	Sequence 4, Appl
26	469.5	55.2	278	19	US-09-581-976-21	Sequence 21, Appl
27	469.5	55.2	278	24	US-10-000-903-21	Sequence 21, Appl
28	469.5	55.2	383	19	US-09-581-976-23	Sequence 23, Appl
29	469.5	55.2	383	24	US-10-000-903-23	Sequence 23, Appl
30	460.5	54.1	158	1	PCT-US00-33549-51	Sequence 51, Appl
31	441.5	51.9	155	1	PCT-US00-33549-63	Sequence 63, Appl
32	332	39.0	236	1	PCT-US00-25559-157	Sequence 157, App
33	332	39.0	236	20	US-09-664-225-157	Sequence 157, App
34	332	39.0	237	1	PCT-US00-25559-158	Sequence 158, App
35	332	39.0	237	20	US-09-664-225-158	Sequence 158, App
36	332	39.0	261	1	PCT-US00-25559-160	Sequence 160, App
37	332	39.0	261	20	US-09-664-225-160	Sequence 160, App
38	331	38.9	117	1	PCT-US00-25559-126	Sequence 126, App
39	331	38.9	117	20	US-09-664-225-126	Sequence 126, App
40	321	37.6	150	1	PCT-US00-33549-6	Sequence 6, Appl
41	320	37.6	150	1	PCT-US00-33549-15	Sequence 15, Appl
42	320	37.6	368	14	US-09-000-004-20	Sequence 20, Appl
43	320	37.6	375	14	US-09-000-004-22	Sequence 22, Appl
44	320	37.6	465	14	US-09-000-004-24	Sequence 24, Appl
45	320	37.6	1587	14	US-09-000-004-46	Sequence 46, Appl

## ALIGNMENTS

RESULT 1

US-09-701-080A-18

Sequence 18, Application US/09701080A

GENERAL INFORMATION:

APPLICANT: O'CONNOR, MARK J.

APPLICANT: ZIMMERMAN, HOLGER

TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P30

FILE REFERENCE: 117-328

CURRENT APPLICATION NUMBER: US/09/701,080A

CURRENT FILING DATE: 2001-02-27

PRIOR APPLICATION NUMBER: GB 9811303.8

PRIOR FILING DATE: 1998-05-26

PRIOR APPLICATION NUMBER: GB 9900157.0

PRIOR FILING DATE: 1999-01-05

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 18

LENGTH: 151

TYPE: PRT

ORGANISM: Human Papillomavirus

US-09-701-080A-18

Query Match

Best Local Similarity 100.0%: Score 851; DB 21; Length 151;

Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MFQDPERRKLPQLCTELQTHIHILCEVCYCKOOLLRREYDFARLDICIVYRDGNPY 60

|||||

Db 1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOOLLREYVDFARFDCIYVRDGNPY 60  
QY 61 AVCDKCLFKFSKYSEYRHYCYSLVGTLLLEOYNNPLCDLLIRNCINCKPLCPPEKORHLD 120  
Db 61 AVCDKCLFKFSKYSEYRHYCYSLVGTLLLEOYNNPLCDLLIRNCINCKPLCPPEKORHLD 120  
QY 121 KKORFNHNRGRWGTGRMCSRSSRTRETOL 151  
Db 121 KKORFNHNRGRWGTGRMCSRSSRTRETOL 151

RESULT 2  
PCT-US00-33549-31  
Sequence 31, Application PC/TUS0033549

GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Cells, Esteban  
APPLICANT: Grey, Howard M.  
APPLICANT: Eplimmune Inc.  
TITLE OF INVENTION: Inducing Cellular Immune Responses to Human  
TITLE OF INVENTION: Papillomavirus Using Peptide and Nucleic Acid  
FILE REFERENCE: 018623-016110PC  
CURRENT APPLICATION NUMBER: PCT/US00/33549  
CURRENT FILING DATE: 2000-12-11  
PRIOR FILING DATE: 1999-12-10  
PRIOR APPLICATION NUMBER: US 60/172,705  
PRIOR FILING DATE: 1999-12-10  
PRIOR APPLICATION NUMBER: US 09/641,528  
NUMBER OF SEQ ID NOS: 86  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 31  
LENGTH: 158  
TYPE: PRT  
ORGANISM: Human papillomavirus type 16  
PCT-US00-33549-31

Query Match 99.1%; Score 843; DB 1; Length 158;  
Best Local Similarity 99.3%; Pred. No. 7.3e-80;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOOLLREYVDFARFDCIYVRDGNPY 60  
Db 8 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOOLLREYVDFARFDCIYVRDGNPY 67  
QY 61 AVCDKCLFKFSKYSEYRHYCYSLVGTLLLEOYNNPLCDLLIRNCINCKPLCPPEKORHLD 120  
Db 68 AVCDKCLFKFSKYSEYRHYCYSLVGTLLLEOYNNPLCDLLIRNCINCKPLCPPEKORHLD 127  
QY 121 KKORFNHNRGRWGTGRMCSRSSRTRETOL 151  
Db 128 KKORFNHNRGRWGTGRMCSRSSRTRETOL 158

RESULT 3  
US-09-980-523A-2  
Sequence 2, Application US/09980523A

GENERAL INFORMATION:  
APPLICANT: CHOPIN, JEANNINE  
APPLICANT: BOURGAULT VILLADA, ISABELLE  
APPLICANT: GUILLET, JEAN-GERARD  
APPLICANT: CONNAN, FRANCES  
APPLICANT: FERRIES, ESTELLE  
TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7  
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE  
FILE REFERENCE: WO/98-01015  
CURRENT APPLICATION NUMBER: US/09/980,523A  
CURRENT FILING DATE: 2002-04-29  
PRIOR APPLICATION NUMBER: PCT/FR00/01513

PRIOR FILING DATE: 2000-05-31  
PRIOR APPLICATION NUMBER: FR 99/07012  
PRIOR FILING DATE: 1999-06-03  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 2  
LENGTH: 158  
TYPE: PRT  
ORGANISM: Human Papillomavirus  
US-09-980-523A-2

Query Match 99.1%; Score 843; DB 23; Length 158;  
Best Local Similarity 99.3%; Pred. No. 1.4e-79;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOOLLREYVDFARFDCIYVRDGNPY 60  
Db 8 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOOLLREYVDFARFDCIYVRDGNPY 67  
QY 61 AVCDKCLFKFSKYSEYRHYCYSLVGTLLLEOYNNPLCDLLIRNCINCKPLCPPEKORHLD 120  
Db 68 AVCDKCLFKFSKYSEYRHYCYSLVGTLLLEOYNNPLCDLLIRNCINCKPLCPPEKORHLD 127  
QY 121 KKORFNHNRGRWGTGRMCSRSSRTRETOL 151  
Db 128 KKORFNHNRGRWGTGRMCSRSSRTRETOL 158

RESULT 4  
US-09-581-976-4  
Sequence 4, Application US/09581976

GENERAL INFORMATION:  
APPLICANT: Dalemans, Wilfried L.J.  
APPLICANT: Gerard, Catherine Marie Ghislaine  
TITLE OF INVENTION: Vaccine  
FILE REFERENCE: B45124  
CURRENT APPLICATION NUMBER: US/09/581,976  
CURRENT FILING DATE: 2000-06-20  
PRIOR APPLICATION NUMBER: PCT/EP98/08563  
PRIOR FILING DATE: 1998-12-18  
PRIOR APPLICATION NUMBER: GB 9727262.9  
PRIOR FILING DATE: 1997-12-24  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 273  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Chimeric protein (protein D from Haemophilus  
OTHER INFORMATION: Influenza B and E6 from Human papilloma virus type  
OTHER INFORMATION: 16)  
US-09-581-976-4

Query Match 99.1%; Score 843; DB 19; Length 273;  
Best Local Similarity 99.3%; Pred. No. 1.4e-79;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOOLLREYVDFARFDCIYVRDGNPY 60  
Db 114 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOOLLREYVDFARFDCIYVRDGNPY 173  
QY 61 AVCDKCLFKFSKYSEYRHYCYSLVGTLLLEOYNNPLCDLLIRNCINCKPLCPPEKORHLD 120  
Db 174 AVCDKCLFKFSKYSEYRHYCYSLVGTLLLEOYNNPLCDLLIRNCINCKPLCPPEKORHLD 233  
QY 121 KKORFNHNRGRWGTGRMCSRSSRTRETOL 151  
Db 234 KKORFNHNRGRWGTGRMCSRSSRTRETOL 264

RESULT 5  
US-10-000-903-4

```
; Sequence 4, Application US/10000903
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 971953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match          99.1%; Score 843; DB 24; Length 273;
Best Local Similarity 99.3%; Pred. No. 1.4e-79;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERRPKLPOLCTELQTTIHDIILCEVCYCKOOLLREVVDFAFRDLCIYRDGNPY 60
DB 114 MFODPOERRPKLPOLCTELQTTIHDIILCEVCYCKOOLLREVVDFAFRDLCIYRDGNPY 173
QY 61 AVCDKCLFKFSKSEYRHCYSLYGTTLEQYNNKPLCDLLIRINCOKPLCEPKORHLD 120
DB 174 AVCDKCLFKFSKSEYRHCYSLYGTTLEQYNNKPLCDLLIRINCOKPLCEPKORHLD 233
QY 121 KKORFHNIRGWTGRCMSCRSSRTRRETOL 151
DB 234 KKORFHNIRGWTGRCMSCRSSRTRRETOL 264

RESULT 6
US-09-581-976-10
; Sequence 10, Application US/09581976
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/09/581,976
; CURRENT FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Chafficial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (Clyta from Streptococcus
; OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-09-581-976-10

Query Match          99.1%; Score 843; DB 19; Length 292;
Best Local Similarity 99.3%; Pred. No. 1.5e-79;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERRPKLPOLCTELQTTIHDIILCEVCYCKOOLLREVVDFAFRDLCIYRDGNPY 60
DB 133 MFODPOERRPKLPOLCTELQTTIHDIILCEVCYCKOOLLREVVDFAFRDLCIYRDGNPY 192
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QY 61 AVCDKCLFKFSKSEYRHCYSLYGTTLEQYNNKPLCDLLIRINCOKPLCEPKORHLD 120
DB 193 AVCDKCLFKFSKSEYRHCYSLYGTTLEQYNNKPLCDLLIRINCOKPLCEPKORHLD 252
QY 121 KKORFHNIRGWTGRCMSCRSSRTRRETOL 151
DB 253 KKORFHNIRGWTGRCMSCRSSRTRRETOL 283

RESULT 7
US-10-000-903-10
; Sequence 10, Application US/10000903
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 971953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-10

Query Match          99.1%; Score 843; DB 24; Length 292;
Best Local Similarity 99.3%; Pred. No. 1.5e-79;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERRPKLPOLCTELQTTIHDIILCEVCYCKOOLLREVVDFAFRDLCIYRDGNPY 60
DB 133 MFODPOERRPKLPOLCTELQTTIHDIILCEVCYCKOOLLREVVDFAFRDLCIYRDGNPY 192
QY 61 AVCDKCLFKFSKSEYRHCYSLYGTTLEQYNNKPLCDLLIRINCOKPLCEPKORHLD 120
DB 193 AVCDKCLFKFSKSEYRHCYSLYGTTLEQYNNKPLCDLLIRINCOKPLCEPKORHLD 252
QY 121 KKORFHNIRGWTGRCMSCRSSRTRRETOL 151
DB 253 KKORFHNIRGWTGRCMSCRSSRTRRETOL 283

RESULT 8
US-09-581-976-6
; Sequence 6, Application US/09581976
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/09/581,976
; CURRENT FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: Chimeric protein (protein D from Haemophilus  
; OTHER INFORMATION: Influenza B and E6E7 fusion from Human papilloma  
; OTHER INFORMATION: virus type 16)  
US-09-581-976-6

Query Match 99.1%; Score 843; DB 19; Length 371;  
Best Local Similarity 99.3%; Pred. No. 2e-79;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOLLRRVYDFAFRDLCIYRDGMPY 60  
DB 114 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOLLRRVYDFAFRDLCIYRDGMPY 173  
QY 61 AVCDKCLFEYSKYSEYRHYCYSLYGTLLLEOQYNKPLCDLLIRINCINOKPLCPPEKORHLD 120  
DB 174 AVCDKCLFEYSKYSEYRHYCYSLYGTLLLEOQYNKPLCDLLIRINCINOKPLCPPEKORHLD 233  
QY 121 KQRFNHNIRGWTGRMCSGCCSSSRTRETOL 151  
DB 234 KQRFNHNIRGWTGRMCSGCCSSSRTRETOL 264

RESULT 9  
; Sequence 6, Application US/10000903

GENERAL INFORMATION:  
; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabezon Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Fernande  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Bencheikh, Angela  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45107  
; CURRENT APPLICATION NUMBER: US/10/000, 903  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: GB 9717953.5  
; PRIOR FILING DATE: 1997-08-22  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 371  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-000-903-6

Query Match 99.1%; Score 843; DB 24; Length 371;  
Best Local Similarity 99.3%; Pred. No. 2e-79;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOLLRRVYDFAFRDLCIYRDGMPY 60  
DB 114 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOLLRRVYDFAFRDLCIYRDGMPY 173  
QY 61 AVCDKCLFEYSKYSEYRHYCYSLYGTLLLEOQYNKPLCDLLIRINCINOKPLCPPEKORHLD 120  
DB 174 AVCDKCLFEYSKYSEYRHYCYSLYGTLLLEOQYNKPLCDLLIRINCINOKPLCPPEKORHLD 233  
QY 121 KQRFNHNIRGWTGRMCSGCCSSSRTRETOL 151  
DB 234 KQRFNHNIRGWTGRMCSGCCSSSRTRETOL 264

RESULT 10  
US-09-581-976-14  
; Sequence 14, Application US/09581976  
; GENERAL INFORMATION:  
; APPLICANT: Dalemans, Wilfried L.J.  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45124  
; CURRENT APPLICATION NUMBER: US/09/581, 976

CURRENT FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: PCT/EP98/08563  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: GB 9727262.9  
; PRIOR FILING DATE: 1997-12-24  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chimeric protein (Clyta from Streptococcus  
; OTHER INFORMATION: pneumoniae and E6E7 fusion from Human papilloma  
; OTHER INFORMATION: virus type 16)  
US-09-581-976-14

Query Match 99.1%; Score 843; DB 19; Length 390;  
Best Local Similarity 99.3%; Pred. No. 2.1e-79;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOLLRRVYDFAFRDLCIYRDGMPY 60  
DB 133 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOLLRRVYDFAFRDLCIYRDGMPY 192  
QY 61 AVCDKCLFEYSKYSEYRHYCYSLYGTLLLEOQYNKPLCDLLIRINCINOKPLCPPEKORHLD 120  
DB 193 AVCDKCLFEYSKYSEYRHYCYSLYGTLLLEOQYNKPLCDLLIRINCINOKPLCPPEKORHLD 252  
QY 121 KQRFNHNIRGWTGRMCSGCCSSSRTRETOL 151  
DB 253 KQRFNHNIRGWTGRMCSGCCSSSRTRETOL 283

RESULT 11  
US-10-000-903-14

GENERAL INFORMATION:  
; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabezon Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Fernande  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Bencheikh, Angela  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45107  
; CURRENT APPLICATION NUMBER: US/10/000, 903  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: GB 9717953.5  
; PRIOR FILING DATE: 1997-08-22  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-000-903-14

Query Match 99.1%; Score 843; DB 24; Length 390;  
Best Local Similarity 99.3%; Pred. No. 2.1e-79;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOLLRRVYDFAFRDLCIYRDGMPY 60  
DB 133 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOLLRRVYDFAFRDLCIYRDGMPY 192  
QY 61 AVCDKCLFEYSKYSEYRHYCYSLYGTLLLEOQYNKPLCDLLIRINCINOKPLCPPEKORHLD 120  
DB 193 AVCDKCLFEYSKYSEYRHYCYSLYGTLLLEOQYNKPLCDLLIRINCINOKPLCPPEKORHLD 252  
QY 121 KQRFNHNIRGWTGRMCSGCCSSSRTRETOL 151

Db 253 KQRFNINRGWTCGMSCCSSRTTRETOL 283

## RESULT 12

US-60-306-809-20  
; Sequence 20, Application US/60306809  
; GENERAL INFORMATION:  
; APPLICANT: SASTRY, K. JAGANNADHA  
; APPLICANT: TORTOLERO-LUNA, GUILERMO  
; APPLICANT: FOLLEN, MICHELE AND COMPOSITIONS RELATING TO HPV-ASSOCIATED  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED  
; FILE REFERENCE: US/60306809  
; CURRENT FILING DATE: 2001-07-20  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 151  
; TYPE: PRT  
; ORGANISM: Human papillomavirus  
US-60-306-809-20

Query Match 98.7%; Score 840; DB 27; Length 151;  
Best Local Similarity 98.7%; Pred. No. 1.4e-79;  
Matches 149; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFQDQERPRKLPOLCTELQTTIHDIIECYCKQOLLREYDFAFRDLCTIYRDNPNY 60  
DB 1 MFQDQERPRKLPOLCTELQTTIHDIIECYCKQOLLREYDFAFRDLCTIYRDNPNY 60  
QY 61 AVCDKCLKFSYSEYRHHYCSLYGTTLEQYNNKPLCDLLIRINCINOKPLCEPEKORHLD 120  
DB 61 AVCDKCLKFSYSEYRHHYCSLYGTTLEQYNNKPLCDLLIRINCINOKPLCEPEKORHLD 120

QY 121 KQRFNINRGWTCGMSCCSSRTTRETOL 151  
DB 121 KQRFNINRGWTCGMSCCSSRTTRETOL 151

## RESULT 13

US-60-415-929-13  
; Sequence 13, Application US/60415929  
; GENERAL INFORMATION:  
; APPLICANT: Cassetti, Maria  
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS  
; FILE REFERENCE: 0630/OM137-USO  
; CURRENT FILING DATE: 2002-10-03  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patent In version 3.1  
; SEQ ID NO 13  
; LENGTH: 151  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
US-60-415-929-13

Query Match 98.7%; Score 840; DB 27; Length 151;  
Best Local Similarity 98.7%; Pred. No. 1.4e-79;  
Matches 149; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFQDQERPRKLPOLCTELQTTIHDIIECYCKQOLLREYDFAFRDLCTIYRDNPNY 60  
DB 1 MFQDQERPRKLPOLCTELQTTIHDIIECYCKQOLLREYDFAFRDLCTIYRDNPNY 60  
QY 61 AVCDKCLKFSYSEYRHHYCSLYGTTLEQYNNKPLCDLLIRINCINOKPLCEPEKORHLD 120  
DB 61 AVCDKCLKFSYSEYRHHYCSLYGTTLEQYNNKPLCDLLIRINCINOKPLCEPEKORHLD 120

QY 121 KQRFNINRGWTCGMSCCSSRTTRETOL 151  
DB 121 KQRFNINRGWTCGMSCCSSRTTRETOL 151

## RESULT 14

US-60-415-929-1  
; Sequence 1, Application US/60415929  
; GENERAL INFORMATION:  
; APPLICANT: Cassetti, Maria  
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS  
; FILE REFERENCE: 0630/OM137-USO  
; CURRENT FILING DATE: 2002-10-03  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patent In version 3.1  
; SEQ ID NO 1  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
US-60-415-929-1

Query Match 98.7%; Score 840; DB 27; Length 248;  
Best Local Similarity 98.7%; Pred. No. 2.6e-79;  
Matches 149; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFQDQERPRKLPOLCTELQTTIHDIIECYCKQOLLREYDFAFRDLCTIYRDNPNY 60  
DB 1 MFQDQERPRKLPOLCTELQTTIHDIIECYCKQOLLREYDFAFRDLCTIYRDNPNY 60  
QY 61 AVCDKCLKFSYSEYRHHYCSLYGTTLEQYNNKPLCDLLIRINCINOKPLCEPEKORHLD 120  
DB 61 AVCDKCLKFSYSEYRHHYCSLYGTTLEQYNNKPLCDLLIRINCINOKPLCEPEKORHLD 120

QY 121 KQRFNINRGWTCGMSCCSSRTTRETOL 151  
DB 121 KQRFNINRGWTCGMSCCSSRTTRETOL 151

## RESULT 15

US-60-415-929-7  
; Sequence 7, Application US/60415929  
; GENERAL INFORMATION:  
; APPLICANT: Cassetti, Maria  
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS  
; FILE REFERENCE: 0630/OM137-USO  
; CURRENT FILING DATE: 2002-10-03  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patent In version 3.1  
; SEQ ID NO 7  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
US-60-415-929-7

Query Match 98.1%; Score 835; DB 27; Length 248;  
Best Local Similarity 98.7%; Pred. No. 8.7e-79;  
Matches 148; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FQDQERPRKLPOLCTELQTTIHDIIECYCKQOLLREYDFAFRDLCTIYRDNPNY 61  
DB 99 FQDQERPRKLPOLCTELQTTIHDIIECYCKQOLLREYDFAFRDLCTIYRDNPNY 158  
QY 62 VCDKCLKFSYSEYRHHYCSLYGTTLEQYNNKPLCDLLIRINCINOKPLCEPEKORHLD 121  
DB 159 VCDKCLKFSYSEYRHHYCSLYGTTLEQYNNKPLCDLLIRINCINOKPLCEPEKORHLD 218  
QY 122 KQRFNINRGWTCGMSCCSSRTTRETOL 151  
DB 219 KQRFNINRGWTCGMSCCSSRTTRETOL 248

Search completed: December 13, 2002, 08:44:50  
Job time : 253.902 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 13, 2002, 08:36:20 ; Search time 3.82822 Seconds  
(without alignments)  
645.878 Million cell updates/sec

Title: US-09-701-080C-1  
Perfect score: 39  
Sequence: 1 XXXXXCPXCXX 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.todent:\*  
12: sp.virus:\*  
13: sp.vertibrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriap:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	79.5	255	10 Q9FRJ9	Q9FRJ9 oryza sativ
2	31	79.5	367	1 Q59667	Q59667 pyrococcus
3	31	79.5	367	17 Q9VOC2	Q9VOC2 pyrococcus
4	31	79.5	367	17 Q8U2E5	Q8U2E5 pyrococcus
5	31	79.5	369	1 Q9UWQ9	Q9UWQ9 thermococcu
6	31	79.5	508	5 Q9XTT3	Q9XTT3 caenorhabdi
7	31	79.5	552	16 Q97EE3	Q97EE3 caenorhabdi
8	30	76.9	119	5 Q9XWV9	Q9XWV9 caenorhabdi
9	30	76.9	144	16 Q9KJ22	Q9KJ22 vibrio chol
10	30	76.9	148	17 Q9YFK5	Q9YFK5 aetopyrum p
11	30	76.9	157	5 Q9BIM1	Q9BIM1 giardia lam
12	30	76.9	165	3 Q12157	Q12157 saccharomyc
13	30	76.9	198	16 Q9KVL1	Q9KVL1 vibrio chol
14	30	76.9	204	10 Q9JUL6	Q9JUL6 arabidopsis
15	30	76.9	210	10 Q9FHG8	Q9FHG8 arabidopsis
16	30	76.9	214	11 Q9DIY0	Q9DIY0 mus musculu

17	30	76.9	232	11 Q9CYU1	Q9CYU1 mus musculu
18	30	76.9	238	10 Q8S2K2	Q8S2K2 oryza sativ
19	30	76.9	238	12 Q8UZN7	Q8UZN7 tobacco str
20	30	76.9	238	12 Q8UYC4	Q8UYC4 tobacco str
21	30	76.9	240	12 Q91MM4	Q91MM4 lumby skin
22	30	76.9	247	4 Q15262	Q15262 homo sapien
23	30	76.9	258	4 Q9NMW3	Q9NMW3 homo sapien
24	30	76.9	297	12 Q9YK65	Q9YK65 melanoplus
25	30	76.9	300	17 Q97OR9	Q97OR9 sulfobolus
26	30	76.9	300	17 Q97YV0	Q97YV0 sulfobolus
27	30	76.9	306	17 Q9HM25	Q9HM25 thermoplasm
28	30	76.9	306	17 Q97C08	Q97C08 thermoplasm
29	30	76.9	329	3 Q9P7F8	Q9P7F8 schizosach
30	30	76.9	335	17 Q27446	Q27446 methanobact
31	30	76.9	343	10 Q9C9X1	Q9C9X1 arabidopsis
32	30	76.9	343	11 Q9DBH5	Q9DBH5 mus musculu
33	30	76.9	348	17 Q50099	Q50099 pyrococcus
34	30	76.9	349	10 Q9SU06	Q9SU06 arabidopsis
35	30	76.9	352	17 Q27796	Q27796 methanobact
36	30	76.9	356	10 Q9XJ08	Q9XJ08 oryza sativ
37	30	76.9	362	10 Q9M2E6	Q9M2E6 arabidopsis
38	30	76.9	376	10 Q9FL07	Q9FL07 arabidopsis
39	30	76.9	379	10 Q93YQ5	Q93YQ5 arabidopsis
40	30	76.9	381	10 Q9CAM6	Q9CAM6 arabidopsis
41	30	76.9	381	10 Q93Z65	Q93Z65 arabidopsis
42	30	76.9	406	10 Q9LR95	Q9LR95 arabidopsis
43	30	76.9	407	10 Q9C965	Q9C965 arabidopsis
44	30	76.9	408	10 Q9LN71	Q9LN71 arabidopsis
45	30	76.9	452	4 Q9NMA5	Q9NMA5 homo sapien

## ALIGNMENTS

RESULT 1  
Q9FRJ9 PRELIMINARY: PRT: 255 AA.  
AC Q9FRJ9: 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Putative ring finger protein.  
GN OSJNB0064P21.7.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. NIPPONBARE;  
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,  
RA Zismann V., Pal G., Bowman C.L., Fujii C.Y., VanAken S.E.,  
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblum T.V.,  
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;  
FT "Oryza sativa chromosome 10 BAC OSJNB0064P21 genomic sequence.";  
RL Submitted (Aug-2001) to the EMBL/GenBank/DBS databases.  
CC -i- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
DR EMBL; AC073166; AAG46117.1; -  
DR InterPro; IPR001841; Znf.Fing.  
DR Pfam; PF00097; zfc3HC4; 1.  
DR SMART; SM00184; RING; 1.  
KW Zinc-finger.  
SQ SEQUENCE 255 AA: 25099 MW: 6F994C3C/987412 CRC64;

Query Match 79.5%; Score 31; DB 10; Length 255;  
Best local similarity 57.1%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
DB 193 NSSCPSC 199

RESULT 2  
059667 PRELIMINARY: PRT: 367 AA.  
AC 059667;  
DT 01-NOV-1996 (TREMblrel. 01, Created)  
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE Hydrogenase (alpha subunit) (EC 1.12.2.1).  
GN HYD (ALPHA SUBUNIT).  
OS Pyrococcus furiosus.  
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
OC Pyrococcus.  
OX NCBI\_TaxID=2261;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-DSM 3638;  
RX MEDLINE=95219100; PubMed=7704275;  
RA Pedroni P., Della Volpe A., Galli G., Mura G.M., Pratesi C.,  
RA Grandi G.;  
RT "Characterization of the locus encoding the [Ni-Fe] sulfhydrogenase  
from the archaeon Pyrococcus furiosus: evidence for a relationship to  
bacterial sulfate reductases";  
RL Microbiology 141:449-458(1995).  
DR EMBL: X75255; CAA53034.1; -;  
DR InterPro: IPR001450; 4Fe4S\_Ferredoxin.  
DR Pfam: PF00037; fer4; 1.  
DR PROSITE: PS00198; 4Fe4S\_FERREDOXIN; 2.  
KW Oxidoreductase.  
SQ SEQUENCE 367 AA; 43398 MW; 9E1509580310330 CRC64;

Query Match 79.5%; Score 31; DB 1; Length 367;  
Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
DB 240 NTTCPTC 246  
RESULT 3  
09VOC2 PRELIMINARY: PRT: 367 AA.  
AC 09VOC2;  
DT 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
DE Hydrogenase (EC 1.12.2.1) (Cytochrome-C3 hydrogenase beta chain).  
GN PAB1784.  
OS Pyrococcus abyssi.  
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
OC Pyrococcus.  
OX NCBI\_TaxID=29292;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-ORSAY;  
RA Heilig R.;  
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome  
structure and evolution";  
RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ248285; CAB49782.1; -;  
DR InterPro: IPR001450; 4Fe4S\_Ferredoxin.  
DR PROSITE: PS00198; 4Fe4S\_FERREDOXIN; 2.  
KW Complete proteome.  
SQ SEQUENCE 367 AA; 43230 MW; 7D2F51C7F846BC0C CRC64;

Query Match 79.5%; Score 31; DB 17; Length 367;  
Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
DB 240 NTTCPTC 246

RESULT 4  
0802E5 PRELIMINARY: PRT: 367 AA.  
AC 0802E5;  
DT 01-JUN-2002 (TREMblrel. 21, Created)  
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)  
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
DE Sulfhydrogenase beta subunit.  
GN PF0891.  
OS Pyrococcus furiosus.  
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
OC Pyrococcus.  
OX NCBI\_TaxID=2261;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-VCI / DSM 3638 / ATCC 43587 / JCM 8422;  
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;  
RT "The complete sequence of the Pyrococcus furiosus genome";  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF010204; AAL81015.1; -;  
KW Complete proteome.  
SQ SEQUENCE 367 AA; 43398 MW; 8329F3842C8C48D0 CRC64;

Query Match 79.5%; Score 31; DB 17; Length 367;  
Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
DB 240 NTTCPTC 246  
RESULT 5  
09UWQ9 PRELIMINARY: PRT: 369 AA.  
AC 09UWQ9;  
DT 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE Nife hydrogenase beta subunit.  
GN HYD.  
OS Thermococcus litoralis.  
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
OC Thermococcus.  
OX NCBI\_TaxID=2265;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-DSM 4573;  
RX MEDLINE=20050631; PubMed=10583413;  
RA Rakhely G., Zhou Z.Z., Adams M.W.W., Kovacs K.L.;  
RT "Biochemical and molecular characterization of the [Nife] hydrogenase  
from the hyperthermophilic archaeon, Thermococcus litoralis";  
RL Eur. J. Biochem. 266:1158-1165(1999).  
DR EMBL: AF039208; AAB94933.1; -;  
DR InterPro: IPR001450; 4Fe4S\_Ferredoxin.  
DR Pfam: PF00037; fer4; 1.  
DR PROSITE: PS00198; 4Fe4S\_FERREDOXIN; 2.  
SQ SEQUENCE 369 AA; 43293 MW; 42332F8B7D749973 CRC64;

Query Match 79.5%; Score 31; DB 1; Length 369;  
Best Local Similarity 57.1%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
DB 242 NTTCPTC 248  
RESULT 6  
09XTT3 PRELIMINARY: PRT: 508 AA.  
ID 09XTT3

AC Q9XWT3;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
 DE Y49E10.20 protein.  
 GN Y49E10.20.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OC NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Barlow K.;  
 RL Submitted (Aug-1997) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99069613; PubMed=9851916;  
 none;  
 RT "Genome sequence of the nematode C.elegans: A platform for  
 RT Investigating biology."  
 RL Science 287:2012-2018(1998).  
 DR EMBL; Z98866; CAB11566.2; -;  
 DR InterPro: IPR002159; CD36; 1.  
 DR Pfam; PF01130; CD36; 1.  
 DR PRINTS; PR01609; CD36FAMILY.  
 SQ SEQUENCE 508 AA; 57287 MW; 5A7078A78F599806 CRC64;

Query Match 79.5%; Score 31; DB 5; Length 508;  
 Best Local Similarity 57.1%; Pred. No. 2e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
 Db 135 NASCPXC 141

RESULT 7  
 O97EE3  
 ID O97EE3 PRELIMINARY; PRT; 552 AA.  
 AC O97EE3;  
 DT 01-OCT-2001 (TREMBLrel. 18, Created)  
 DT 01-OCT-2001 (TREMBLrel. 18, last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
 DE Dihydroxy-acid dehydratase.  
 GN CAC3170.  
 OS Clostridium acetobutylicum.  
 OC Bacteria; Firmicutes; Bacillales; Clostridium group; Clostridia;  
 OC Clostridiales; Clostridiaceae; Clostridium.  
 OC NCBI\_TaxID=1488;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;  
 RX MEDLINE=2159325; PubMed=11466286;  
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,  
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hittl J., Wolf Y.I.,  
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,  
 RA Bennett G.N., Koonin E.V., Smith D.R.,  
 "Genome sequence and comparative analysis of the solvent-producing  
 RT bacterium Clostridium acetobutylicum";  
 RL J. Bacteriol. 183:4823-4838(2001).  
 DR EMBL; AE007812; AAK81107.1; -;  
 DR InterPro: IPR004404; ILVD.  
 DR InterPro: IPR000581; ILVD\_EDD\_family.  
 DR Pfam; PF00920; ILVD\_EDD; 1.  
 DR ProDom; PD002691; ILVD\_EDD\_family; 1.  
 DR TIGRFAMS; TIGR00110; ILVD; 1.  
 DR PROSITE; PS00886; ILVD\_EDD\_1; 1.  
 DR PROSITE; PS00887; ILVD\_EDD\_2; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 552 AA; 58366 MW; 9309A73FE7CD81F5 CRC64;

Query Match 79.5%; Score 31; DB 16; Length 552;  
 Best Local Similarity 57.1%; Pred. No. 2e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 OY 4 NXXCPXC 10  
 Db 182 NTACPTC 188

RESULT 8  
 O9XWV9  
 ID O9XWV9 PRELIMINARY; PRT; 119 AA.  
 AC O9XWV9;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)  
 DE T28C6.8 protein.  
 GN T28C6.8.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OC NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lloyd C.R.;  
 RL Submitted (SEP-1995) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99069613; PubMed=9851916;  
 none;  
 RT "Genome sequence of the nematode C.elegans: A platform for  
 RT Investigating biology."  
 RL Science 287:2012-2018(1998).  
 DR EMBL; Z54238; CAA90999.2; -;  
 SQ SEQUENCE 119 AA; 13204 MW; E7127E4547880432 CRC64;

Query Match 76.9%; Score 30; DB 5; Length 119;  
 Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
 Db 8 NUSCPAC 14

RESULT 9  
 O9KJL2  
 ID O9KJL2 PRELIMINARY; PRT; 144 AA.  
 AC O9KJL2;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
 DE Thioresdoxin 2.  
 GN VCA0752.  
 OS Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.  
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.  
 OC NCBI\_TaxID=666;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=EL TOR N16961 / SEROTYPE O1;  
 RX MEDLINE=20406833; PubMed=10952301;  
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,  
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,  
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,  
 RA Ermolaeva M.D., Yamathayan J., Bass S., Qin H., Dragoi I., Sellers P.,  
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,  
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,  
 Fraser C.M.;  
 "DNA sequence of both chromosomes of the cholera pathogen Vibrio  
 RT cholerae";  
 RL Nature 406:477-483(2000).  
 DR EMBL; AE004403; AAF96650.1; -;  
 DR HSSP; P80579; IQOW.  
 DR TIGR; VCA0752; -;  
 DR InterPro: IPR000063; Thioresdoxin.

DR Pfam; PF00085; thired.1.  
 DR PRINTS; PR00421; THIOREDOXIN.  
 DR TIGRFAMs; TIGR01068; thiredoxin.1.  
 KW Complete proteome.  
 SQ SEQUENCE 144 AA; 15968 MW; 9997AF6744A84CA5 CRC64;

Query Match 76.9%; Score 30; DB 16; Length 144;  
 Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPC 10  
 | | | |  
 Db 5 NTRCPC 11

## RESULT 10

O9YFK5 PRELIMINARY; PRT; 148 AA.

AC O9YFK5;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Hypothetical protein APE0243.  
 GN APE0243.  
 OS Aeropyrum pernix.  
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcates;  
 OC Desulfurococcaceae; Aeropyrum.  
 OX NCBI\_TaxID=56636;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K1;  
 RX MEDLINE=99310339; PubMed=10382966;  
 RA Kwarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Halkawa Y.,  
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Anki A., Kosugi H.,  
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,  
 RA Takamizawa M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,  
 RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,  
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.,  
 RT "Complete genome sequence of an aerobic hyper-thermophilic  
 RT crenarchaeon, Aeropyrum pernix K1.",  
 RL DNA Res. 6:83-101(1999)  
 DR EMBL; AP000058; BAK79156.1; -.  
 DR InterPro: IPR000063; Thired.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 148 AA; 16500 MW; 263AEBD8E893D7F CRC64;

Query Match 76.9%; Score 30; DB 17; Length 148;  
 Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPC 10  
 | | | |  
 Db 50 NALCPAC 56

## RESULT 11

O9BIM1 PRELIMINARY; PRT; 157 AA.

AC O9BIM1;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Variable surface protein 7b (Fragment).  
 OS Giardia lamblia (Giardia intestinalis).  
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.  
 OX NCBI\_TaxID=5741;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21391783; PubMed=11500396;  
 RA Blenz M., Siles-lucas M., Wittwer P., Muller N.;  
 RT "vsp Gene Expression by Giardia lamblia Clone GS/M-83-H7 during  
 RT Antigenic Variation in Vivo and in Vitro.",  
 RL Infect. Immun. 69:5278-5285(2001).

DR EMBL; AF354520; AAK31225.1; -.  
 DR InterPro: IPR005127; Giardia\_vsp.  
 DR Pfam; PF03302; VSP.1.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 157 AA; 15872 MW; 8C370EF98907D76B CRC64;

Query Match 76.9%; Score 30; DB 5; Length 157;  
 Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPC 10  
 | | | |  
 Db 44 NGSCPAC 50

## RESULT 12

O12157 PRELIMINARY; PRT; 165 AA.

AC O12157;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Chromosome IV reading frame ORF YDL008W.  
 GN APC11 OR D2900 OR YDL008W.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Urrestarazu L.A., Andre B., Vissers S.;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MIPS;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ALPHA S288C;  
 RA Andre B., Vissers S., Urrestarazu L.;  
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Z74056; CAA98564.1; -.  
 DR EMBL; Z48432; CAA86351.1; -.  
 DR SGD; S0002166; APC11.  
 DR InterPro: IPR001841; Znf\_ring.  
 DR SMART; SM00184; RING; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 165 AA; 18865 MW; 99F8E8C6BC841934 CRC64;

Query Match 76.9%; Score 30; DB 3; Length 165;  
 Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPC 10  
 | | | |  
 Db 49 NGTCCPC 55

## RESULT 13

O9KVL1 PRELIMINARY; PRT; 198 AA.

AC O9KVL1;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Hypothetical protein VC0131.  
 GN VC0131.  
 OS Vibrrio cholerae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrrio.  
 OX NCBI\_TaxID=666;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-EL TOR N16961 / SEROTYPE O1;  
 RX MEDLINE=20406833; PubMed=10952301;  
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,  
 RA Dodson R.J., Hatt D.H., Hickey E.K., Peterson J.D., Umayam L.A.,  
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,  
 RA Ermlaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,  
 RA McDonald L., Ullrich T., Fleischmann R.D., Nierman W.C., White O.,  
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,  
 RA Fraser C.M.,  
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio  
 RT cholerae";  
 RL Nature 406:477-483(2000).  
 DR EMBL: AE004103; AF93308.1;  
 DR TIGR: VC0131;  
 DR InterPro: IPR000152; ASX\_HYDROXYL.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 198 AA; 22841 MW; C139FCACAE26F3A7 CRC64;

Query Match 76.9%; Score 30; DB 16; Length 198;  
 Best Local Similarity 57.1%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
 DB 2 NACCPDC 8

RESULT 14

Q9JUL6 PRELIMINARY; PRT; 204 AA.

AC Q9JUL6;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Similarity to RING-H2 zinc finger protein ATL3.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-COLUMBIA;  
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 RM [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-COLUMBIA;  
 RX MEDLINE=20277480; PubMed=10819329;  
 RA Nakamura Y.;  
 RT Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence  
 RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC  
 RT clones.";  
 RL DNA Res. 7:131-135(2000).  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL: AB022220; BAB01038.1;  
 DR InterPro: IPR001841; Znf\_ring.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00184; RING; 1.  
 KW zinc-finger.  
 SQ SEQUENCE 204 AA; 22859 MW; 90FC33157DA90D25 CRC64;

Query Match 76.9%; Score 30; DB 10; Length 204;  
 Best Local Similarity 57.1%; Pred. No. 1.8e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
 DB 123 NSTCPLC 129

RESULT 15

Q9FHG8 PRELIMINARY; PRT; 210 AA.

AC Q9FHG8;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Similarity to C3HC4-type RING zinc finger protein.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-COLUMBIA;  
 RX MEDLINE=99397451; PubMed=10470850;  
 RA Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,  
 RA Miyajima N., Tabata S.;  
 RL "Structural analysis of Arabidopsis thaliana chromosome 5. IX.  
 RL Sequence features of the regions of 1,011,550 bp covered by seventeen  
 RL P1 and TAC clones.";  
 RL DNA Res. 6:183-195(1999).  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL: AB018118; BAB09593.1;  
 DR InterPro: IPR001841; Znf\_ring.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00184; RING; 1.  
 KW zinc-finger.  
 SQ SEQUENCE 210 AA; 23523 MW; E27A1C1A75CC77A6 CRC64;

Query Match 76.9%; Score 30; DB 10; Length 210;  
 Best Local Similarity 57.1%; Pred. No. 1.8e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
 DB 157 NSTCPLC 163

Search completed: December 13, 2002, 08:39:37  
 Job time : 6.82822 secs

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102(a)

1/99

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OM protein - protein search, using sw model

Run on: December 13, 2002, 08:31:40 : Search time 1.25153 Seconds

(without alignments)  
397.685 Million cell updates/sec

Title: US-09-701-080C-1

Perfect score: 39

Sequence: 1 XXXNXXCPXCXX 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : SWISSProt\_40 : \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	79.5	286	1	ILVD_CLOPA
2	31	79.5	552	1	ILVD_CLOAB
3	30	76.9	113	1	HYBF_PROVU
4	30	76.9	237	1	COAT_TOBSV
5	30	76.9	290	1	LEP4_PSEAE
6	30	76.9	547	1	YDRD_SCHPO
7	30	76.9	600	1	RNI2_MOUSE
8	30	76.9	612	1	EXO2_BPT5
9	30	76.9	624	1	RNI2_HUMAN
10	30	76.9	627	1	ASM_MOUSE
11	30	76.9	634	1	SYLA_AQUAE
12	30	76.9	745	1	HGL2_ARATH
13	30	76.9	810	1	NEI1_HUMAN
14	30	76.9	810	1	NEI1_RAT
15	30	76.9	816	1	NEI2_HUMAN
16	30	76.9	816	1	NEI2_MOUSE
17	30	76.9	816	1	NEI2_RAT
18	30	76.9	816	1	NEI2_CHICK
19	30	76.9	894	1	SYLM_SACDO
20	30	76.9	894	1	SYLM_YEAST
21	30	76.9	994	1	SYLM_NEUCR
22	30	76.9	1115	1	PAN2_YEAST
23	29	74.4	92	1	RLA4_HALMA
24	29	74.4	93	1	VEB5_LAMBD
25	29	74.4	97	1	VE7_HPV33
26	29	74.4	118	1	LSHB_PHYCA
27	29	74.4	128	1	LSHB_PHOSU
28	29	74.4	138	1	LSHB_CANPA
29	29	74.4	141	1	LSHB_CERST
30	29	74.4	141	1	LSHB_PIG
31	29	74.4	143	1	LSHB_FELCA
32	29	74.4	166	1	YAA3_HAEIN
33	29	74.4	209	1	YE28_AQUAE

34	29	74.4	233	1	HOXU_ALCEU	P22318 alcaligenes
35	29	74.4	281	1	VNS1_INBAC	P13883 influenza b
36	29	74.4	281	1	VNS1_INBGA	P12592 influenza b
37	29	74.4	281	1	VNS1_INBHK	P12594 influenza b
38	29	74.4	281	1	VNS1_INBID	P12596 influenza b
39	29	74.4	281	1	VNS1_INBSJ	P12601 influenza b
40	29	74.4	281	1	VNS1_INBYA	P12602 influenza b
41	29	74.4	281	1	VNS1_INBYA	P08013 influenza b
42	29	74.4	333	1	Y808_METJA	O58218 methanococc
43	29	74.4	377	1	RNG1_HUMAN	O06587 homo sapien
44	29	74.4	421	1	REF1_METJA	O58239 methanococc
45	29	74.4	459	1	ZPR1_MOUSE	O62384 mus musculu

## ALIGNMENTS

RESULT 1	ILVD_CLOPA	STANDARD:	PRT:	286 AA.
ID	ILVD_CLOPA			
AC	P31959			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Dihydroxy-acid dehydratase (EC 4.2.1.9) (DAD) (Fragment).			
GN	ILVD.			
OS	Clostridium pasteurianum.			
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;			
OX	Clostridium.			
OX	NCBI_TaxID=1501;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94227243; PubMed=8173074;			
RA	Oultram J.D., Loughlin M., Wainman S.M., Gunner S.M., Minton N.P.;			
RT	"The nucleotide sequence of genes involved in the leucine biosynthetic pathway of Clostridium pasteurianum."			
RL	DNA Seq. 4:105-111(1993).			
CC	- CATALYTIC ACTIVITY: 2,3-dihydroxy-3-methylbutanoate -> 3-methyl-2-oxobutanoate + H2O.			
CC	- CORFACTOR: BINDS 1 4FE-4S CLUSTER (POTENTIAL).			
CC	- PATHWAY: Valine and isoleucine biosynthesis; fourth step.			
CC	- SIMILARITY: BELONGS TO THE ILVD / EDD FAMILY.			
CC	-----			
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CC	-----			
DR	EMBL: L06666; AAC41395.1; .			
DR	InterPro: IPR000581; ILVD_EDD_family.			
DR	Pfam: PF00920; ILVD_EDD_1.			
DR	ProDom: PD002691; ILVD_EDD_family; 1.			
DR	PROSITE: PS00886; ILVD_EDD_2; PARTIAL.			
DR	PROSITE: PS00887; ILVD_EDD_1; 1.			
FT	Branch-chain amino acid biosynthesis; Lyase; Iron-sulfur; 4Fe-4S.			
KW	METAL			
FT	METAL 119 119			
FT	METAL 191 191			
FT	NON_TER 286 286			
SO	SEQUENCE 286 AA; 29925 MW; 7CF6655CCEFF927 CRC64;			
Query Match	Score 31; DB 1; Length 286;			
Best Local Similarity	57.1%; Pred. No. 60;			
Matches	4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
OY	4 NXXCPXC 10			
DB	182 NXXCPXC 188			
RESULT 2				

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ILVD_CLOAB
ID ILVD_CLOAB STANDARD; PRT; 552 AA.
AC 097EE3;
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Dihydroxy-acid dehydratase (EC 4.2.1.9) (DAD).
GN ILVD OR CAC3170.
OS Clostridium acetobutylicum.
OC Bacteria: Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium
OX NCBI_TaxID=1488;
RN
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; Pubmed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hiltl J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum."
RL J. Bacteriol. 183:4823-4838(2001).
CC -1- CATALYTIC ACTIVITY: 2,3-dihydroxy-3-methylbutanoate = 3-methyl-2-
CC Oxobutanate + H(2)O.
CC -1- COFACTOR: Binds 1 4Fe-4S cluster (Potential).
CC -1- PATHWAY: Valine and isoleucine biosynthesis; fourth step.
CC -1- SIMILARITY: BELONGS TO THE ILVD / EDD FAMILY.
CC -----
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CC -----
DR EMBL; AE007812; AAK81107.1; -.
DR InterPro; IPR004404; ILVD.
DR InterPro; IPR000581; ILVD_EDD_family.
DR Pfam; PF00920; ILVD_EDD_1.
DR Prodom; PD002691; ILVD_EDD_family; 1.
DR TIGRFAMs; TIGR00110; ILVD_1.
DR DR PROSITE; PS00886; ILVD_EDD_1; 1.
DR PROSITE; PS00887; ILVD_EDD_2; 1.
DR KW Branched-chain amino acid biosynthesis; Lyase; Iron-sulfur; 4Fe-4S;
KW Complete proteome.
FT METAL 119 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT METAL 191 IRON-SULFUR (4FE-4S) (POTENTIAL).
SQ SEQUENCE 552 AA; 58366 MW; 9309A73FE7CD81F5 CRC64;
Query Match 79.5%; Score 31; DB 1; Length 552;
Best Local Similarity 57.1%; Pred. No. 93;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 NXXCPXC 10
Db 182 NTACPTC 188

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88004470; Pubmed=3308458;
RA Cole S.T.;
RT "Nucleotide sequence and comparative analysis of the ftd operon
RT encoding the fumarate reductase of Proteus vulgaris. Extensive
RT sequence divergence of the membrane anchors and absence of an
RT ftd-linked ampc cephalosporinase gene."
RL Eur. J. Biochem. 167:481-488(1987).
CC -1- FUNCTION: PROBABLY PLAYS A ROLE IN AN HYDROGENASE NICKEL COFACTOR
CC INSERTION STEP.
CC -1- SIMILARITY: BELONGS TO THE HYPA/HYBF FAMILY.
CC -----
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CC -----
DR EMBL; X06151; CAA29510.1; -.
DR PIR; S00118; S00118.
DR InterPro; IPR000688; HyPA.
DR Pfam; PF01155; HyPA; 1.
DR Prodom; PD003620; HyPA; 1.
DR TIGRFAMs; TIGR00100; hyPa; 1.
DR PROSITE; PS01249; HyPA; 1.
KW Metal-binding; Nickel.
FT METAL 2 NICKEL (POTENTIAL).
FT METAL 73 NICKEL (POTENTIAL).
FT METAL 76 NICKEL (POTENTIAL).
FT METAL 89 NICKEL (POTENTIAL).
FT METAL 92 NICKEL (POTENTIAL).
SQ SEQUENCE 113 AA; 12619 MW; 17CAD773C6A1B2DD CRC64;
Query Match 76.9%; Score 30; DB 1; Length 113;
Best Local Similarity 57.1%; Pred. No. 46;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 NXXCPXC 10
Db 86 MAGCPAC 92

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RESULT 3
HYBF_PROVU
ID HYBF_PROVU STANDARD; PRT; 113 AA.
AC P20926;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable hydrogenase nickel incorporation protein hybf.
GN HYBF.
OS Proteus vulgaris.
OC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=585;

```

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RESULT 4
COAT_TOBSV
ID COAT_TOBSV STANDARD; PRT; 237 AA.
AC F03598;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Coat protein (p4 protein).
OS Tobacco streak virus (strain WC) (TSV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Ilarivirus.
OX NCBI_TaxID=12318;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=84169544; Pubmed=6546793;
RA Cornelissen B.J.C., Janssen H., Zuidema D., Bol J.F.;
RT "Complete nucleotide sequence of tobacco streak virus RNA 3."
RL Nucleic Acids Res. 12:2427-2437(1984).
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CC -----
DR EMBL; X00435; CAA25133.1; -.

```



DR PIR: A04206; VCBWVC.  
 DR InterPro: IPR002681; Ila1r-coat.  
 DR Pfam: PF01787; Ila1r-coat.1.  
 SQ SEQUENCE 237 AA; 26237 MW; E1FF87AE7102523 CRC64;

Query Match 76.9%; Score 30; DB 1; Length 237;  
 Best Local Similarity 57.1%; Pred. No. 76;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
 DB 25 NSRCPTC 31

RESULT 5  
 LEPA\_PSEAE STANDARD; PRT; 290 AA.  
 ID LEPA\_PSEAE  
 AC P22610;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Type 4, prepilin-like proteins leader peptide processing enzyme  
 DE (protein secretion protein XCPA) (PILD protein). [Includes: Leader  
 DE peptidase (EC 3.4.99.-) (Prepilin peptidase); N-methyltransferase  
 DE (EC 2.1.1.-)].  
 GN PILD OR XCPA OR PA4528.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 OC Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PAK:  
 RX MEDLINE=90264276; PubMed=1971619;  
 RA Nunn D., Bergman S., Lory S.;  
 RT "Products of three accessory genes, pilB, pilC, and pILD, are  
 RT required for biogenesis of Pseudomonas aeruginosa pili.";  
 RL J. Bacteriol. 172:2911-2919(1990).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 15692 / PA01;  
 RX MEDLINE=91100333; PubMed=1898929;  
 RA Bally M., Ball G., Badere A., Lazdunski A.;  
 RT "Protein secretion in Pseudomonas aeruginosa: the xcpA gene encodes  
 RT an integral inner membrane protein homologous to Klebsiella  
 RT pneumoniae secretion function protein Pilo.";  
 RL J. Bacteriol. 173:479-486(1991).  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 15692 / PA01;  
 RX MEDLINE=20437337; PubMed=10984043;  
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,  
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Garber R.L., Goltz L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
 RT opportunistic pathogen.";  
 RL Nature 406:959-964(2000).  
 RN (4)  
 RP REVIEW.  
 RX MEDLINE=97368114; PubMed=9224881;  
 RA Lory S., Strom M.S.;  
 RT "Structure-function relationship of type-IV prepilin peptidase of  
 RT Pseudomonas aeruginosa -- a review.";  
 RL Gene 192:117-121(1997).  
 RN (5)  
 RP REVIEW.  
 RX MEDLINE=94335721; PubMed=8057924;  
 RA Strom M.S., Nunn D.N., Lory S.;  
 RT "Posttranslational processing of type IV prepilin and homologs by PILD  
 RT of Pseudomonas aeruginosa.";

RL Meth. Enzymol. 235:527-540(1994).  
 RN [6]  
 RP MUTAGENESIS OF CYSTEINE RESIDUES.  
 RX MEDLINE=93340186; PubMed=8340405;  
 RA Strom M.S., Bergman P., Lory S.;  
 RT "Identification of active-site cysteines in the conserved domain of  
 RT PILD, the bifunctional type IV pilin leader  
 RT peptidase/N-methyltransferase of Pseudomonas aeruginosa.";  
 RL J. Biol. Chem. 268:15788-15794(1993).  
 RN [7]  
 RP MUTAGENESIS OF GLY-95 AND LYS-96.  
 RX MEDLINE=98334648; PubMed=9668097;  
 RA Pepe J.C., Lory S.;  
 RT "Amino acid substitutions in pILD, a bifunctional enzyme of  
 RT Pseudomonas aeruginosa. Effect on leader peptidase and  
 RT N-methyltransferase activities in vitro and in vivo.";  
 RL J. Biol. Chem. 273:19120-19129(1998).  
 CC -I- FUNCTION: CLEAVES TYPE-4 FIMBRIAL LEADER SEQUENCE AND METHYLATES  
 CC THE N-TERMINAL (GENERALLY PHE) RESIDUE. PROCESSES THE PILIN  
 CC PRECURSOR DURING MEMBRANE TRANSLOCATION. REQUIRED FOR THE ASSEMBLY  
 CC OF TYPE IV PILI AND FOR SECRETION OF MOST PROTEINS.  
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.  
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A24.  
 CC -----  
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 CC -----  
 DR EMBL: M32066; AAA25734.1; -  
 DR EMBL: M61096; AAA26023.1; -  
 DR EMBL: AE004867; AAG07916.1; -  
 DR PIR: C35384; C35384.  
 DR PIR: A39131; A39131.  
 DR MEROPS: A24.001; -  
 DR InterPro: IPR000045; Peptidase\_C20.  
 DR Pfam: PF01478; Peptidase\_C20; I.  
 DR PRINTS: PR00864; PREPILNPTASE.  
 KW Multifunctional enzyme; Hydrolase; Protease; Transferase;  
 KW Methyltransferase; Transmembrane; Inner membrane; Complete proteome.  
 FT TRANSMEM 13  
 FT DOMAIN 34  
 FT TRANSMEM 127  
 FT TRANSMEM 128  
 FT TRANSMEM 158  
 FT TRANSMEM 163  
 FT TRANSMEM 203  
 FT TRANSMEM 228  
 FT TRANSMEM 248  
 FT TRANSMEM 261  
 FT ACT\_SITE 72  
 FT ACT\_SITE 75  
 FT ACT\_SITE 97  
 FT ACT\_SITE 100  
 FT ACT\_SITE 100  
 FT VARIANT 18  
 FT VARIANT 18  
 SO SEQUENCE 290 AA; 31870 MW; 57A8526EB18FB752 CRC64;  
 Query Match 76.9%; Score 30; DB 1; Length 290;  
 Best Local Similarity 57.1%; Pred. No. 87;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
 DB 69 NSACPCX 75

RESULT 6  
 YDRD\_SCHPO STANDARD; PRT; 547 AA.  
 ID YDRD\_SCHPO  
 AC O13747;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)



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OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC T5-like viruses.
OX NCBI_TaxID=10726;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89057468; PubMed=3057441;
RA Kallman A.V., Kryukov V.M., Bayer A.A.;
RT "The nucleotide sequence of the region of bacteriophage T5 early
RT genes D10-D15."
RL Nucleic Acids Res. 16:10353-10354(1988).
RN [2]
RP POSSIBLE FUNCTION.
RX MEDLINE=89338712; PubMed=2547651;
RA Blinov V.M., Koonin E.V., Gorbalevskaya A.E., Kallman A.V., Kryukov V.M.;
RT "Two early genes of bacteriophage T5 encode proteins containing an
RT NTP-binding sequence motif and probably involved in DNA replication,
RT recombination and repair."
RL FEBS Lett. 252:47-52(1989).
CC -1- FUNCTION: POSSIBLE EXONUCLEASE INVOLVED IN PHAGE DNA
CC RECOMBINATION, REPLICATION, AND REPAIR.
CC -1- SUBUNIT: COULD CONSIST OF TWO SUBUNITS: D13 AND D12.
CC -1- SIMILARITY: STRONG TO T4 PROTEIN GP46.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X12930; CAA31400.1; -.
DR EMBL: X12930; CAA31401.1; ALT_INIT.
DR EMBL: AJ001191; CAA04586.1; -.
DR FIR: S01933; M0BPT5.
DR InterPro: IPR003439; ABC_transport.
DR Hydrolyase; Nuclease; Exonuclease; ATP-binding; DNA repair;
KW Early protein.
FT NP_BIND 35 42 ATP (POTENTIAL).
SQ SEQUENCE 612 AA; 68673 MW; 92E7B652D1DE141 CRC64;

Query Match
Best Local Similarity 76.9%; Score 30; DB 1; Length 612;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10
DB 306 NTECPYC 312

RESULT 9
RN12_HUMAN
ID RN12_HUMAN STANDARD: PRT; 624 AA.
AC Q9NWV2; Q9Y598;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE RING finger protein 12 (LIM domain interacting RING finger protein)
DE (RING finger LIM domain-binding protein) (R-LIM) (NY-RFN-43 antigen).
GN RNF12 OR LIM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20469411; PubMed=11013082;
RA Ostendorf H.P., Bossenz M., Mincheva A., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Lichter P., Bach I.;
RT "Functional characterization of the gene encoding RLIM, the
RT corepressor of LIM homeodomain transcription factors."
RL Genomics 69:120-130(2000).
RN [2]

```

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RP SEQUENCE FROM N.A.
RC TISSUE=renal cell carcinoma;
RX MEDLINE=99438124; PubMed=10508479;
RA Scanlan M.J., Jordan J.D., Williamson B., Stockert E., Bander N.H.,
RA Jungeneel V., Gure A.O., Jager D., Jager E., Knuth A., Chen Y.-T.,
RA Old L.;
RT "Antigens recognized by autologous antibody in patients with renal-
RT cell carcinoma."
RL Int. J. Cancer 83:456-464(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Magatsuma M., Hosoi T., Raku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.,
RA Nimomiya K., Iwayanagi T.;
RT "NED0 human cDNA sequencing project."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ACTS AS A NEGATIVE CO-REGULATOR FOR LIM HOMEODOMAIN
CC TRANSCRIPTION FACTORS. VIA THE RECRUITMENT OF THE SIN3A/HISTONE
CC DEACETYLASE COREPRESSOR COMPLEX.
CC -1- SUBUNIT: ASSOCIATES WITH LIM/HOMEOBOX FACTORS.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANY TISSUES.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to frameshifts
CC in position 134 and 142.
CC -----
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CC -----
DR EMBL: AJ271670; CAC14228.1; -.
DR EMBL: AF155109; AAD42875.1; ALT_FRAME.
DR EMBL: AK001334; BAA91632.1; -.
DR Genew; HGNC:13429; RNF12.
DR MIM: 300379; -.
DR InterPro: IPR001841; ZNF_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING_1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Transcription regulation; Zinc-finger.
FT DOMAIN 422 506
FT ZN_FING 570 611
FT DOMAIN 453 481
FT DOMAIN 500 506
FT CONFLICT 126 126
FT CONFLICT 134 134
FT CONFLICT 144 145
FT CONFLICT 418 418
SQ SEQUENCE 624 AA; 68527 MW; DE3ADE09ACAC8CF8 CRC64;

Query Match
Best Local Similarity 76.9%; Score 30; DB 1; Length 624;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10
DB 604 NSTCPYC 610

RESULT 10
RN12_MOUSE
ID RN12_MOUSE STANDARD: PRT; 627 AA.
AC Q04519;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
RN [2]

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DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE sphingomyelin phosphodiesterase precursor (EC 3.1.4.12) (acid  
 sphingomyelinase) (asmase).  
 GN SMPD1 OR ASM.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C; TISSUE=Liver;  
 RX MEDLINE=93183402; PubMed=1292508;  
 RA Mirczella D., Stoffel W.;  
 RT "Molecular cloning of the acid sphingomyelinase of the mouse and the  
 organization and complete nucleotide sequence of the gene.";  
 RL Biol. Chem. Hoppe-Seyler 373:1233-1238(1992).  
 RN [2]  
 RP REVISIONS TO 224-225 AND 384.  
 RA Hofmann K.;  
 RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: CONVERTS SPHINGOMYELIN TO CERAMIDE. ASM ALSO HAS  
 CC PHOSPHOLIPASE C ACTIVITIES TOWARD 1,2-DIACYLGLYCEROLPHOSPHOCHOLINE  
 CC AND 1,2-DIACYLGLYCEROLPHOSPHOGLYCEROL.  
 CC -1- CATALYTIC ACTIVITY: Sphingomyelin + H(2)O = N-acetylphingosine +  
 CC choline phosphate.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Lysosomal.  
 CC -1- MISCELLANEOUS: THERE ARE TWO TYPES OF SPHINGOMYELINASES: ASM  
 CC (ACID), AND NSM (NEUTRAL).  
 CC -1- SIMILARITY: BELONGS TO THE ACID SPHINGOMYELINASE FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 SAPOSIN B-TYPE DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL: Z14252; CAAT78619.1; -  
 DR EMBL: Z14132; CAAT78506.1; -  
 DR EMBL: BC011304; AAH11304.1; -  
 DR PIR: S27392; S27392.  
 DR PIR: S27393; S27393.  
 DR MGD: MGI:98325; Smpd1.  
 DR InterPro: IPR004843; M-peptidase.  
 DR InterPro: IPR004844; S/T-phosphatase.  
 DR InterPro: IPR000004; Saph.  
 DR Pfam: PF00149; Metallophos; 1.  
 DR SMART: SM00118; SAPB; 1.  
 KW Hydrolase; Glycosidase; Lysosome; Glycoprotein; Signal.  
 FT SIGNAL 1 44  
 FT CHAIN 45 627 SPHINGOMYELIN PHOSPHODIESTERASE.  
 FT DOMAIN 83 167 SAPOSIN-LIKE TYPE B.  
 FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 518 518 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 48 48 S -> T (IN REF. 3).  
 FT CONFLICT 450 450 G -> S (IN REF. 3).  
 SQ SEQUENCE 627 AA: 65922 MW: 0PFC7EA74EB71B91 CRC64;

Query Match 76.9%; Score 30; DB 1; Length 627;  
 Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
 DB 84 NLTCPAC 90  
 RESULT 11  
 ID SYLA\_AQUAE STANDARD; PRT; 634 AA.  
 AC 066680;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DE 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE leucyl-tRNA synthetase alpha subunit (EC 6.1.1.4) (Leucine--tRNA  
 DE ligase alpha subunit) (LeuRS).  
 GN LEUS OR AQ\_351.  
 OS Aquifex aeolicus.  
 OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;  
 OC Aquifex.  
 OX NCBI\_TaxID=63363;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-VF5;  
 RX MEDLINE=98196666; PubMed=9537320;  
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,  
 RA Graham D.E., Overbeek R., Shead M.A., Keller M., Aujay M., Huber R.,  
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;  
 RT "The complete genome of the hyperthermophilic bacterium Aquifex  
 RT aeolicus.";  
 RL Nature 392:353-358(1998).  
 CC -1- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP +  
 CC diphosphate + L-leucyl-tRNA(Leu).  
 CC -1- SUBUNIT: SEEMS TO CONSIST OF AN ALPHA CHAIN AND A BETA CHAIN.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AE000685; AAC06643.1; -  
 DR HSSP: P96142; IGAX.  
 DR InterPro: IPR002302; Leu-tRNAsynlla.  
 DR InterPro: IPR002300; tRNA-synt\_1a.  
 DR InterPro: IPR001412; tRNA-synt\_1.  
 DR Pfam: PF00133; tRNA-synt\_1; 1.  
 DR PRINTS: PR00985; TRNASYNTHLEU.  
 DR TIGRFAMS: TIGR00396; leus\_bact; 1.  
 DR PROSITE: PS00178; AA\_tRNA\_LIGASE\_1; 1.  
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;  
 KW Complete proteome.  
 FT SITE 43 51 "HIGH" REGION.  
 FT SITE 43 51  
 SQ SEQUENCE 634 AA: 73989 MW: 0119CA3F7A018766 CRC64;

Query Match 76.9%; Score 30; DB 1; Length 634;  
 Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 NXXCPXC 10  
 DB 501 NLTCPAC 507  
 RESULT 12  
 ID HGL2\_ARATH STANDARD; PRT; 745 AA.  
 AC P46607; Q39018;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Homeobox protein GLABRA2 (Homeobox-leucine zipper protein ATHB-10)  
 DE (HD-ZIP protein ATHB-10).  
 GN GL2 OR AT1G79840 OR F19K16.20.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.  
 NC NCBITaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Wassilewskija; TISSUE=Seedling;  
 RX MEDLINE=95011550; PubMed=7926739;  
 RA Rerie W.G., Feldmann K.A., Marks M.D.;  
 RT "The GLABRA2 gene encodes a homeo domain protein required for normal  
 RL trichome development in Arabidopsis.",  
 RN Genes Dev. 8:1388-1399(1994).  
 RP REVISIONS.  
 RA Marks M.D.;  
 RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=96407838; PubMed=8811855;  
 RA di Cristina M., Sessa G., Dolan L., Linstead P., Baima S., Ruberti I.,  
 RA Morelli G.;  
 RT "The Arabidopsis Athb-10 (GLABRA2) is an HD-zip protein required for  
 RL regulation of root hair development.",  
 RL Plant J. 10:393-402(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=21016719; PubMed=11130712;  
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,  
 RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,  
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,  
 RA Dunn P., Elgu P., Feldhym T.V., Feng J.-D., Fong B., Fujii C.Y.,  
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,  
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
 RA Kim C.U., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,  
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Mafti R., Marzilli A.,  
 RA Miltischer J., Miranda M., Nguyen M., Niemman W.C., Osborne B.I.,  
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
 RA Sun H., Tallon L.J., Tambunga G., Tortum M.J., Town C.D.,  
 RA Uterback T., Van Aken S., Vayenberg M., Vysotskaia V.S., Walker M.,  
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;  
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
 RL thaliana".  
 RL Nature 408:816-820(2000).  
 CC -1- FUNCTION: REQUIRED FOR CORRECT MORPHOLOGICAL DEVELOPMENT AND  
 CC MATURATION OF TRICHOES AS WELL AS FOR NORMAL DEVELOPMENT OF SEED  
 CC COAT MUCIAGE.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING TRICHOES.  
 CC -1- SIMILARITY: BELONGS TO THE HD-ZIP HOMEBOX FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 START DOMAIN.  
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 CC -----  
 CC EMBL: L32873; AAC80260.1; -  
 CC EMBL: Z54356; CAA91183.1; ALT\_INIT.  
 CC EMBL: AC011717; AAG52245.1; -  
 CC HSP: P01367; IAPL.

DR TRANSFAC; T02961; -  
 DR InterPro: IPR001356; Homeobox.  
 DR InterPro: IPR002913; START.  
 DR Pfam: PF00046; homeobox\_1.  
 DR Pfam: PF01852; START\_1.  
 DR ProDom: PD000010; Homeobox; 1.  
 DR SMART: SM00389; HOX; 1.  
 DR SMART: SM00234; START; 1.  
 DR PROSITE: PS00027; HOMEBOX\_1; 1.  
 DR PROSITE: PS00071; HOMEBOX\_2; 1.  
 DR PROSITE: PS00848; START; 1.  
 KW Homeobox; DNA-binding; Nuclear protein.  
 FT DOMAIN 248 487 START.  
 FT DOMAIN 39 60 ASP/GLU-RICH (ACIDIC).  
 FT DOMAIN 70 87 ASP/GLU-RICH (ACIDIC).  
 FT DNA\_BIND 99 158 HOMEBOX.  
 SQ SEQUENCE 745 AA; 82988 MW; E4AD2DAC15D5F3 CRC64;  
 Query Match 76.9%; Score 30; DB 1; Length 745;  
 Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 NXXCPXC 10  
 Db 188 NSCPC 194  
 RESULT 13  
 ID NEIL\_HUMAN  
 AC 092832; Q9Y472;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Protein kinase C-binding protein NEIL1 precursor (NEIL-like protein 1)  
 DE (NEIL-related protein 1).  
 GN NEIL1 OR NRPL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBITaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=97131504; PubMed=8975702;  
 RA Watanabe T.K., Katagiri T., Suzuki M., Shimizu F., Fujiwara T.,  
 RA Kanemoto N., Nakamura Y., Hirai Y., Maekawa H., Takahashi E.;  
 RT "Cloning and characterization of two novel human cDNAs (NEIL1 and  
 RL NEIL2) encoding proteins with six EGF-like repeats.";  
 RL Genomics 38:273-276(1996).  
 RN [2]  
 RP SEQUENCE OF 383-910 FROM N.A.  
 RA Ting K., Vastardis H., Mulliken J.B., Bertolami C., Wen Z.,  
 RA Young M., Tieu A., Kwong E.;  
 RT "Neil homolog gene expression in craniofacial anomalies.";  
 RL Submitted (Sep-1996) to the EMBL/Genbank/DBJ databases.  
 CC -1- SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1 (BY SIMILARITY).  
 CC -1- DISEASE: EXPRESSED IN CRANIOFACIAL ANOMALIES.  
 CC -1- SIMILARITY: CONTAINS 1 TSP N-TERMINAL DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 5 WFC DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.  
 CC -1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS  
 CC IN POSITIONS 427 AND 771.  
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 CC -----

DR EMBL; D83017; BA11680.1; -.  
 DR EMBL; U57523; AAB06946.1; ALT\_FRAME.  
 DR HSSP; P07204; IADX.  
 DR Genew; HGNC:7750; NEIL1.  
 DR MIM; 602319; -.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001791; Laminin\_G.  
 DR InterPro; IPR003129; TSPN.  
 DR InterPro; IPR001007; VWF\_C.  
 DR Pfam; PF00008; EGF\_4.  
 DR Pfam; PF00093; VWC; 3.  
 DR Pfam; PF02210; TSPN; 1.  
 DR SMART; SM00179; EGF\_Ca; 2.  
 DR SMART; SM00001; EGF\_like; 4.  
 DR SMART; SM00282; LamG; 1.  
 DR SMART; SM00210; TSPN; 1.  
 DR SMART; SM00214; VWC; 3.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 3.  
 DR PROSITE; PS01187; EGF\_Ca; 3.  
 DR PROSITE; PS01208; VWF\_C; 2.  
 DR GlycoProtein; EGF-like domain; Repeat; signal.  
 KW SIGNAL. 1 16  
 FT CHAIN 17 810 POTENTIAL.  
 FT DOMAIN 81 230 PROTEIN KINASE C-BINDING PROTEIN NEIL1.  
 FT DOMAIN 273 331 TSP N-TERMINAL.  
 FT DOMAIN 335 390 VWF\_C 1.  
 FT DOMAIN 391 433 EGF-LIKE 1.  
 FT DOMAIN 434 475 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 476 516 EGF-LIKE 3.  
 FT DOMAIN 515 547 EGF-LIKE 4.  
 FT DOMAIN 549 595 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 596 631 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 632 687 VWF\_C 3.  
 FT DOMAIN 692 750 VWF\_C 4.  
 FT DOMAIN 752 807 VWF\_C 5.  
 FT DISULFID 395 407 BY SIMILARITY.  
 FT DISULFID 401 416 BY SIMILARITY.  
 FT DISULFID 418 432 BY SIMILARITY.  
 FT DISULFID 438 451 BY SIMILARITY.  
 FT DISULFID 445 460 BY SIMILARITY.  
 FT DISULFID 462 474 BY SIMILARITY.  
 FT DISULFID 480 493 BY SIMILARITY.  
 FT DISULFID 487 502 BY SIMILARITY.  
 FT DISULFID 504 515 BY SIMILARITY.  
 FT DISULFID 519 529 BY SIMILARITY.  
 FT DISULFID 523 535 BY SIMILARITY.  
 FT DISULFID 537 546 BY SIMILARITY.  
 FT DISULFID 553 566 BY SIMILARITY.  
 FT DISULFID 560 575 BY SIMILARITY.  
 FT DISULFID 577 594 BY SIMILARITY.  
 FT DISULFID 600 613 BY SIMILARITY.  
 FT DISULFID 607 622 BY SIMILARITY.  
 FT DISULFID 624 630 BY SIMILARITY.  
 FT CARBOHYD 40 40 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 224 224 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 372 372 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 511 511 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 562 562 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 609 609 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 708 708 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 732 732 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 758 758 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 383 383 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CONFLICT 573 573 Y -> D (IN REF. 2).  
 FT CONFLICT 573 573 Y -> H (IN REF. 2).  
 FT CONFLICT 626 626 S -> C (IN REF. 2).  
 SQ SEQUENCE 810 AA: 89606 MW: 549465EA3FAEBD0 CRC64;

Query Match 76.9%; Score 30; DB 1; Length 810;  
 Best Local Similarity 57.1%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXPCX 10  
 Db 224 NHTCPTC 230

RESULT 14  
 NEIL\_RAT  
 ID NEIL\_RAT STANDARD; PRT; 810 AA.  
 AC 062919;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Protein kinase C-binding protein NEIL1 precursor (NEIL-like protein 1).  
 GN NEIL1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxId=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Sprague-Dawley; TISSUE-Brain;  
 RX MEDLINE=20017976; PubMed=10548494;  
 RA Kuroda S., Oyasu M., Kawakami M., Kanayama N., Tanizawa K., Saito N.,  
 RA Abe T., Matsushashi S., Tung K.;  
 RT "Biochemical characterization and expression analysis of neural  
 RT thrombospondin-1-like proteins NEIL1 and NEIL2";  
 RL Biochem. Biophys. Res. Commun. 265:79-86(1999).  
 CC -1- SUBUNIT: HOMODIMER. BINDS TO PKC BETA-1.  
 CC -1- SIMILARITY: CONTAINS 1 TSP N-TERMINAL DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 5 VWF\_C DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.  
 CC  
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 CC -----

DR EMBL; U48246; AAC72252.1; -.  
 DR HSSP; P35355; IEMN.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001791; Laminin\_G.  
 DR InterPro; IPR003129; TSPN.  
 DR InterPro; IPR001007; VWF\_C.  
 DR Pfam; PF00008; EGF\_4.  
 DR Pfam; PF00093; VWC; 3.  
 DR Pfam; PF02210; TSPN; 1.  
 DR SMART; SM00179; EGF\_Ca; 2.  
 DR SMART; SM00001; EGF\_like; 4.  
 DR SMART; SM00282; LamG; 1.  
 DR SMART; SM00210; TSPN; 1.  
 DR SMART; SM00214; VWC; 4.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 3.  
 DR PROSITE; PS01187; EGF\_Ca; 3.  
 DR PROSITE; PS01208; VWF\_C; 2.  
 KW Glycoprotein; EGF-like domain; Repeat; signal.  
 FT SIGNAL 1 16 POTENTIAL.  
 FT CHAIN 17 810 PROTEIN KINASE C-BINDING PROTEIN NEIL1.  
 FT DOMAIN 81 230 TSP N-TERMINAL.  
 FT DOMAIN 273 331 VWF\_C 1.  
 FT DOMAIN 335 390 VWF\_C 2.



FT	DISULFID	606	619	BY SIMILARITY.
FT	DISULFID	613	628	BY SIMILARITY.
FT	DISULFID	630	636	BY SIMILARITY.
FT	CARBOHYD	53	53	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	225	225	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	293	293	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	298	298	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	517	517	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	615	615	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	635	635	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	816 AA;	91346 MM;	89370B987DC7A324 CRC64;

Query Match 76.98; Score 30; DB 1; Length 816;  
 Best Local Similarity 57.18; Pred. No. 1.7e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXGCPXC 10  
 DB 225 NRTCPYC 231

Search completed: December 13, 2002, 08:38:37  
 Job time : 2.25153 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 13, 2002, 08:36:45 ; Search time 1.91411 Seconds  
(without alignments)  
602.689 Million cell updates/sec

Title: US-09-701-080C-1  
Perfect score: 39  
Sequence: 1 XXXNXXCPXCXX 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	79.5	367	2	S48833 cytochrome-c3 hydr
2	31	79.5	367	2	E75133 cytochrome-c3 hydr
3	31	79.5	534	2	T27054 hypothetical prote
4	31	79.5	552	2	H97289 dihydroxy-acid deh
5	30	76.9	113	2	S00118 hypothetical prote
6	30	76.9	117	2	T25411 hypothetical prote
7	30	76.9	117	2	F88765 protein T28C6.8 (l
8	30	76.9	118	2	T27456 hypothetical prote
9	30	76.9	144	2	B82423 thioredoxin 2 VCA0
10	30	76.9	148	2	B72782 hypothetical prote
11	30	76.9	165	2	S52511 hypothetical prote
12	30	76.9	198	2	D82361 conserved hypotet
13	30	76.9	237	1	VC8WMC coat protein - tob
14	30	76.9	280	1	A39131 type IV prepilin p
15	30	76.9	297	2	T28188 hypothetical prote
16	30	76.9	300	2	F90274 pyruvate formate-1
17	30	76.9	335	1	F69052 hypothetical prote
18	30	76.9	343	2	H96703 probable RING zinc
19	30	76.9	348	1	A71012 hypothetical prote
20	30	76.9	349	2	T06680 hypothetical prote
21	30	76.9	352	2	A69103 conserved hypotet
22	30	76.9	362	2	T47910 hypothetical prote
23	30	76.9	381	2	C96657 hypothetical prote
24	30	76.9	407	2	G96835 probable RING zinc
25	30	76.9	495	2	T04466 hypothetical prote
26	30	76.9	544	2	S24915 gene 18 protein -
27	30	76.9	547	2	T37793 probable zinc flng
28	30	76.9	557	2	A48434 variant-specific s
29	30	76.9	612	1	WDBPT5 gene D13 protein -

30	30	76.9	627	1	S27393 splicingmyelin phos
31	30	76.9	634	2	D70331 leucine-trna ligas
32	30	76.9	718	2	T05850 homeobox protein A
33	30	76.9	738	2	E85061 probable homeotic
34	30	76.9	745	2	D96829 homeobox protein (
35	30	76.9	747	2	S71478 homeotic protein A
36	30	76.9	749	2	G86186 hypothetical prote
37	30	76.9	768	2	S71477 homeotic protein,
38	30	76.9	776	2	T20738 hypothetical prote
39	30	76.9	810	2	T10756 ne1-homolog protei
40	30	76.9	812	2	D96979 leucyl-trna synthet
41	30	76.9	835	2	JP0076 ne1 protein - chic
42	30	76.9	894	1	SYBYLM leucine-trna ligas
43	30	76.9	894	1	SYBYMX leucine-trna ligas
44	30	76.9	994	1	SYNCLM leucine-trna ligas
45	30	76.9	1083	2	C88854 protein F11A10.3 l

## ALIGNMENTS

RESULT 1  
S48833  
cytochrome-c3 hydrogenase (EC 1.12.2.1) alpha chain - Pyrococcus furiosus  
C:Species: Pyrococcus furiosus  
C:Date: 10-Dec-1994 #sequence\_revision 13-Mar-1997 #text\_change 09-Jun-2000  
C:Accession: S48833  
R:Pedroni, P.  
submitted to the EMBL Data Library, September 1993  
A:Reference number: S48833  
A:Accession: S48833  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-367 <PEP>  
A:Cross-References: EMBL:X75255; NID:9562773; PID:9563905  
C:Genetics:  
A:Start codon: GTG  
C:Superfamily: Pyrococcus furiosus cytochrome-c3 hydrogenase alpha chain  
C:Keywords: oxidoreductase

Query Match 79.5%; Score 31; DB 2; Length 367;  
Best Local Similarity 57.1%; Pred. No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
DB 240 NTCPTC 246

## RESULT 2

E75133  
cytochrome-c3 hydrogenase (EC 1.12.2.1) beta chain PAB1784 - Pyrococcus abyssi (strai

C:Species: Pyrococcus abyssi  
C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000  
C:Accession: E75133

R:anonymous, Genoscope  
submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s

A:Reference number: A75001  
A:Accession: E75133

A>Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-367 <RAW>  
A:Cross-References: GB:AJ248285; GB:AL096836; NID:95458067; PIDN:CA849782.1; PID:9545

A:Experimental source: strain Orsay  
C:Genetics:  
A:Gene: PAB1784

C:Superfamily: Pyrococcus furiosus cytochrome-c3 hydrogenase alpha chain  
C:Keywords: oxidoreductase

Query Match 79.5%; Score 31; DB 2; Length 367;  
Best Local Similarity 57.1%; Pred. No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
| | |  
Db 240 NTTCPTC 246

## RESULT 3

T27054  
hypothetical protein Y49E10.20 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 17-Mar-2000  
C:Accession: T27054  
R:Barlow, K.  
submitted to the EMBL Data Library, August 1997  
A:Reference number: Z20303  
A:Accession: T27054  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-534 <WIL>  
A:Cross-references: EMBL:Z98866; PIDN:CAB11566.1; GSPDB:GN00021; CESP:Y49E10.20  
C:Genetics:  
A:Experimental source: clone Y49E10  
A:Gene: CESP:Y49E10.20  
A:Map position: 3  
A:Introns: 42/3; 105/2; 188/3; 231/3; 359/1; 440/2; 505/3  
C:Superfamily: lysosomal integral membrane protein II

Query Match 79.5%; Score 31; DB 2; Length 534;  
Best Local Similarity 57.1%; Pred. No. 5.1e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
| | |  
Db 135 NASCPTC 141

## RESULT 4

H97289  
dihydroxy-acid dehydratase [imported] - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C>Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 30-Sep-2001  
C:Accession: H97289  
R:Noiling, J.; Bretton, G.; Omelechenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium CLO  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: H97289  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-552 <KUR>  
A:Cross-references: GB:AE001437; PIDN:AAK81107.1; PID:q15026238; GSPDB:GN00168  
C:Genetics:  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics: CAC3170  
A:Superfamily: dihydroxy-acid dehydratase

Query Match 79.5%; Score 31; DB 2; Length 552;  
Best Local Similarity 57.1%; Pred. No. 5.2e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
| | |  
Db 182 NTACPTC 188

## RESULT 5

S00118  
hypothetical protein B - Proteus vulgaris  
C:Species: Proteus vulgaris  
C>Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 20-Sep-1999  
C:Accession: S00118  
R:Cole, S.T.

Eur. J. Biochem. 167, 481-488, 1987  
A:Title: Nucleotide sequence and comparative analysis of the ftd operon encoding the  
d-linked ampc cephalosporinase gene.  
A:Reference number: S00107; MUID:88004470; PMID:3308458  
A:Accession: S00118  
A:Molecule type: DNA  
A:Residues: 1-113 <COL>  
A:Cross-references: EMBL:X06151; NID:g45907; PIDN:CAA29510.1; PID:g45909  
C:Superfamily: hydrogenase accessory protein

Query Match 76.9%; Score 30; DB 2; Length 113;  
Best Local Similarity 57.1%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
| | |  
Db 86 NACCPAC 92

## RESULT 6

T25411  
hypothetical protein T28C6.8 - Caenorhabditis elegans (fragment)  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T25411  
R:Lloyd, C.  
submitted to the EMBL Data Library, September 1995  
A:Reference number: Z20030  
A:Accession: T25411  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-117 <WIL>  
A:Cross-references: EMBL:Z54238; PIDN:CAA9099.1; GSPDB:GN00022; CESP:T28C6.8  
C:Genetics:  
A:Experimental source: clone T28C6  
A:Gene: CESP:T28C6.8  
A:Map position: 4

Query Match 76.9%; Score 30; DB 2; Length 117;  
Best Local Similarity 57.1%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
| | |  
Db 8 NLSCPAC 14

## RESULT 7

F88765  
protein T28C6.8 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
C:Accession: F88765  
R:anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio  
A:Reference number: A75000; MUID:99069613; PMID:9851916  
A:Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C-  
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;  
A:Accession: F88765  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-117 <STO>  
A:Cross-references: GB:chr\_IV; PIDN:CAA90999.1; PID:g4038509; GSPDB:GN00022; CESP:T28  
C:Genetics:  
A:Gene: T28C6.8  
A:Map position: 4

Query Match 76.9%; Score 30; DB 2; Length 117;  
Best Local Similarity 57.1%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10

Db 8 NMSCPAC 14

RESULT 8  
T27456  
hypothetical protein Y87G2A.d - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T27456  
R:White, S.  
submitted to the EMBL Data Library, September 1999  
A:Reference number: Z20371  
A:Accession: T27456  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-118 <WILD>  
A:Cross-references: EMBL:AL110500; NID:e1542314; PIDN:CAB54478.1; CESP:Y87G2A.d  
A:Experimental source: clone Y87G2A  
C:Genetics:  
A:Gene: CESP:Y87G2A.d  
A:introns: 19/3; 52/3

Query Match  
Best Local Similarity 76.9%; Score 30; DB 2; Length 118;  
Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NMXCPXC 10

Db 102 NMSCPAC 108

RESULT 9  
B82423  
thioredoxin 2 VCA0752 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)  
C:Species: *Vibrio cholerae*  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
C:Accession: B82423  
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.; Chardon, D.; Esmolaeva, M.D.; Yamachevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.  
A:Reference number: AB2035; MUID:20406833; PMID:10952301  
A:Accession: B82423  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-144 <HEI>  
A:Cross-references: GB:AE004403; GB:AE003853; NID:g9658159; PIDN:AAF96650.1; GSPDB:GN001  
A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VCA0752  
A:Map position: 2  
C:Superfamily: thioredoxin; thioredoxin homology

Query Match  
Best Local Similarity 76.9%; Score 30; DB 2; Length 144;  
Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NMXCPXC 10

Db 5 NTRCPSC 11

RESULT 10  
B72782  
hypothetical protein APE0243 - *Aeropyrum pernix* (strain K1)  
C:Species: *Aeropyrum pernix*  
C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jun-2000  
C:Accession: B72782  
R:Kawabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, *Aero*  
A:Reference number: A72450; MUID:99310339; PMID:10382966  
A:Accession: B72782  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-148 <KAW>  
A:Cross-references: DBJ:AP000058; NID:g5103388; PIDN:BA79156.1; PID:d1042932; PID:g  
C:Genetics:  
A:Gene: APE0243  
C:Superfamily: *Aeropyrum pernix* hypothetical protein APE0243

Query Match  
Best Local Similarity 76.9%; Score 30; DB 2; Length 148;  
Pred. No. 3.4e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NMXCPXC 10

Db 50 NALCPAC 56

RESULT 11  
S52511  
hypothetical protein YDL008w - yeast (*Saccharomyces cerevisiae*)  
N:Alternate names: hypothetical protein D2900  
C:Species: *Saccharomyces cerevisiae*  
C:Date: 08-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 19-Apr-2002  
C:Accession: S52511; S67540  
R:Andre, B.; Vissers, S.; Urrestarazu, L.  
submitted to the EMBL Data Library, February 1995  
A:Description: The sequence of a 42 kb segment located on the left arm of chromosome  
A:Reference number: S52492  
A:Accession: S52511  
A:Molecule type: DNA  
A:Residues: 1-165 <AND>  
A:Cross-references: EMBL:Z48432; NID:g683669; PIDN:CA88351.1; PID:g683689  
A:Experimental source: strain S288C  
R:Urrestarazu, L.A.; Andre, B.; Vissers, S.  
submitted to the Protein Sequence Database, July 1996  
A:Reference number: S67535  
A:Accession: S67540  
A:Molecule type: DNA  
A:Residues: 1-165 <URR>  
A:Cross-references: EMBL:Z74056; NID:g1430968; PIDN:CA98564.1; PID:e252972; PID:g143  
A:Experimental source: strain S288C  
C:Genetics:  
A:Gene: SGD:APC11  
A:Cross-references: SGD:S0002166  
A:Map position: 4L

Query Match  
Best Local Similarity 76.9%; Score 30; DB 2; Length 165;  
Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NMXCPXC 10

Db 49 NGTSPSC 55

RESULT 12  
D82361  
conserved hypothetical protein WC0131 [imported] - *Vibrio cholerae* (strain N16961 ser  
C:Species: *Vibrio cholerae*  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Aug-2002  
C:Accession: D82361  
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.  
Chardon, D.; Esmolaeva, M.D.; Yamachevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers  
I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.  
A:Reference number: AB2035; MUID:20406833; PMID:10952301  
A:Accession: D82361  
A:Status: preliminary

A:Molecule type: DNA  
 A:Residues: 1-198 <HEI>  
 A:Cross-references: GB:AE004103; GB:AE003852; NID:9654523; PIDN:AAF93308.1; GSPDB:GN001  
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
 C:Genetics:  
 A:Gene: VC0131  
 A:Map position: 1  
 C:Superfamily: Escherichia coli hypothetical protein b2583

Query Match 76.9%; Score 30; DB 2; Length 198;  
 Best Local Similarity 57.1%; Pred. No. 4e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
 1 111  
 Db 2 NAACPDC 8

#### RESULT 13

VCBVMC  
 coat protein - tobacco streak virus (strain WC)

N:Alternate names: P4 protein

C:Species: tobacco streak virus, TSV

A:Note: host Nicotiana glauca x N. clevelandii (tobacco)

C:Date: 28-Aug-1985 #sequence\_revision 28-Aug-1985 #text\_change 23-Jul-1999

C:Accession: A04206

R:Corneilissen, B.J.C.; Janssen, H.; Zuidema, D.; Bol, J.F.

Nucleic Acids Res. 12, 2427-2437, 1984

A:Title: Complete nucleotide sequence of tobacco streak virus RNA 3.

A:Reference number: A93507; MUID:84169544; PMID:6546793

A:Accession: A04206

A:Molecule type: genomic RNA

A:Residues: 1-237 <COR>

A:Cross-references: GB:X00435; NID:962146; PIDN:CAA2513.1; PID:962148

C:Genetics:

A:Map position: segment 3

C:Superfamily: tobacco streak virus coat protein

Query Match 76.9%; Score 30; DB 1; Length 237;  
 Best Local Similarity 57.1%; Pred. No. 4.4e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
 1 111  
 Db 25 NSRCPTC 31

#### RESULT 14

A39131  
 type IV prepilin peptidase (EC 3.4.99.-) pILD - Pseudomonas aeruginosa

N:Alternate names: inner membrane protein xcpA

C:Species: Pseudomonas aeruginosa

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 31-Dec-2000

C:Accession: A39131; C35384; D83078

R:Bailly, M.; Bail, G.; Badere, A.; Lazdunski, A.

J. Bacteriol. 173, 479-486, 1991

A:Title: Protein secretion in Pseudomonas aeruginosa: the xcpA gene encodes an integral

A:Reference number: A39131; MUID:91100333; PMID:1898929

A:Accession: A39131

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-290 <BAL>

A:Cross-references: GB:M61096; GB:M38720; NID:9151641; PIDN:AAA26023.1; PID:9151642

R:Nunn, D.; Bergman, S.; Lory, S.

J. Bacteriol. 172, 2911-2919, 1990

A:Title: Products of three accessory genes, pilB, pilC, and pILD, are required for bioge

A:Reference number: A35384; MUID:90264276; PMID:1971619

A:Accession: C35384

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-17, 'A', 19-290 <NDN>

A:Cross-references: GB:M32066; NID:9151064; PIDN:AAA25734.1; PID:9151067

A:Note: the authors translated the codon AAC for residue 30 as Ala  
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;  
 Adam, S.; Van, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lartig, K.; L  
 : Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: D83078

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-290 <STO>

A:Cross-references: GB:AE004867; GB:AE004091; NID:9950769; PIDN:AA607916.1; GSPDB:GN

A:Experimental source: strain PA01

C:Genetics:

A:Gene: pILD; xcpA; pILD; PA4528

C:Superfamily: type IV prepilin peptidase

C:Keywords: hydrolase; methyltransferase; S-adenosylmethionine; transmembrane protein

Query Match 76.9%; Score 30; DB 1; Length 290;  
 Best Local Similarity 57.1%; Pred. No. 5e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
 1 111  
 Db 69 NSACPXC 75

#### RESULT 15

T28188  
 hypothetical protein ORF29 - Melanoplus sanguinipes entomopoxvirus (isolate Tuscon)

N:Alternate names: ORF MSV027 tryptophan repeat gene family protein

C:Species: Melanoplus sanguinipes entomopoxvirus

A:Variety: isolate Tuscon

C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 02-Sep-2000

C:Accession: T28188

R:Alonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.

J. Virol. 73, 533-552, 1999

A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.

A:Reference number: 220484; MUID:99102612; PMID:9847359

A:Accession: T28188

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: DNA

A:Residues: 1-297 <AFO>

A:Cross-references: EMBL:AF063866; NID:94049647; PIDN:AA097845.1; PID:94049885

A:Experimental source: isolate Tuscon

C:Genetics:

A:Note: MSV027

C:Superfamily: RING finger homology

F;248-296/Domain: RING finger homology <RRN>

Query Match 76.9%; Score 30; DB 2; Length 297;  
 Best Local Similarity 57.1%; Pred. No. 5.1e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
 1 111  
 Db 284 NSRCPMC 290

Search completed: December 13, 2002, 08:40:10  
 Job time : 4.91411 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 13, 2002, 08:38:45 ; Search time 1.91411 Seconds  
(without alignments)  
420.734 Million cell updates/sec

Title: US-09-701-080C-1

Perfect score: 39

Sequence: 1 XXXNXXCPXCXX 12

Scoring table:

BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 239201 seqs, 67110966 residues

Total number of hits satisfying chosen parameters: 239201

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Pending\_Patents\_AA\_New:\*  
1: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep:\*  
7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	76.9	84	US-09-513-999C-7264	Sequence 7264, App
2	30	76.9	237	US-09-989-733-295	Sequence 295, App
3	30	76.9	237	US-09-992-643-295	Sequence 295, App
4	30	76.9	237	US-10-125-923A-222	Sequence 222, App
5	30	76.9	237	US-10-205-892-222	Sequence 222, App
6	30	76.9	237	US-10-174-575-222	Sequence 222, App
7	30	76.9	237	US-10-174-575-222	Sequence 222, App
8	30	76.9	332	US-09-724-676-78297	Sequence 78297, A
9	30	76.9	332	US-09-724-676-78297	Sequence 78297, A
10	30	76.9	332	US-09-724-676-78297	Sequence 78297, A
11	30	76.9	332	US-09-724-676-78297	Sequence 78297, A
12	30	76.9	332	US-09-724-676-78297	Sequence 78297, A
13	30	76.9	332	US-09-724-676-78297	Sequence 78297, A
14	30	76.9	332	US-09-724-676-78297	Sequence 78297, A
15	30	76.9	332	US-09-724-676-78297	Sequence 78297, A
16	30	76.9	332	US-09-724-676-78297	Sequence 78297, A
17	30	76.9	332	US-09-724-676-78297	Sequence 78297, A
18	30	76.9	332	US-09-724-676-78297	Sequence 78297, A
19	30	76.9	332	US-09-724-676-78297	Sequence 78297, A
20	30	76.9	332	US-09-724-676-78297	Sequence 78297, A
21	30	76.9	332	US-09-724-676-78297	Sequence 78297, A
22	30	76.9	332	US-09-724-676-78297	Sequence 78297, A
23	30	76.9	332	US-09-724-676-78297	Sequence 78297, A
24	30	76.9	332	US-09-724-676-78297	Sequence 78297, A
25	30	76.9	332	US-09-724-676-78297	Sequence 78297, A
26	30	76.9	332	US-09-724-676-78297	Sequence 78297, A

27	29	74.4	113	6	US-10-057-498-26222	Sequence 26222, A
28	29	74.4	136	7	US-60-425-113-49	Sequence 49, Appl
29	29	74.4	139	7	US-60-425-113-49	Sequence 62, Appl
30	29	74.4	297	6	US-10-288-160-8	Sequence 8, Appl
31	29	74.4	358	5	US-09-724-676-71193	Sequence 71193, A
32	29	74.4	358	5	US-09-724-676-71193	Sequence 71193, A
33	29	74.4	368	6	US-10-092-411A-5436	Sequence 5436, Ap
34	29	74.4	452	6	US-10-264-237-2355	Sequence 2355, Ap
35	29	74.4	636	5	US-09-724-676-62863	Sequence 62863, A
36	29	74.4	636	5	US-09-724-676-62863	Sequence 62863, A
37	29	74.4	642	5	US-09-724-676-62864	Sequence 62864, A
38	29	74.4	649	5	US-09-724-676-62864	Sequence 62864, A
39	29	74.4	649	5	US-09-724-676-62864	Sequence 62864, A
40	29	74.4	649	5	US-09-724-676-62864	Sequence 62864, A
41	29	74.4	662	5	US-09-724-676-62865	Sequence 62865, A
42	29	74.4	662	5	US-09-724-676-62865	Sequence 62865, A
43	29	74.4	723	6	US-10-092-411A-5060	Sequence 5060, Ap
44	29	74.4	813	6	US-10-231-778-2	Sequence 2, Appl
45	28	71.8	12	5	US-09-701-080C-1	Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-09-513-999C-7264  
Sequence 7264, Application US/09513999C  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclet, A.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59, US2, REG  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 7264  
LENGTH: 84  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: 16  
OTHER INFORMATION: Xaa-Gly or Arg  
US-09-513-999C-7264

Query Match  
Best Local Similarity 76.9%; Score 30; DB 5; Length 84;  
Matches 4; Conservative 0; Mismatches 3; Indels 0;  
DB 20 NSQCPAC 26

RESULT 2  
US-09-989-733-295  
Sequence 295, Application US/09989733  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.

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: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2730P1C68
: CURRENT APPLICATION NUMBER: US/09/989,733
: CURRENT FILING DATE: 2001-11-01
: PRIOR APPLICATION NUMBER: 60/049787
: PRIOR FILING DATE: 1997-06-16
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/065186
: PRIOR FILING DATE: 1997-11-12
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066770
: PRIOR FILING DATE: 1997-11-24
: PRIOR APPLICATION NUMBER: 60/075945
: PRIOR FILING DATE: 1998-02-25
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/083322
: PRIOR FILING DATE: 1998-04-28
: PRIOR APPLICATION NUMBER: 60/084600
: PRIOR FILING DATE: 1998-05-07
: PRIOR APPLICATION NUMBER: 60/087106
: PRIOR FILING DATE: 1998-05-28
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 532
: SEQ ID NO 295
: LENGTH: 237
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-989-733-295

Query Match
Best Local Similarity 76.9%; Score 30; DB 5; Length 237;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXPCXC 10
      | | |
Db 122 NAECPAC 128

RESULT 3
: Sequence 295, Application US/09992643
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerlitsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kljavin, Ivar J.
```

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: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2730P1C13
: CURRENT APPLICATION NUMBER: US/09/992,643
: CURRENT FILING DATE: 2001-11-01
: PRIOR APPLICATION NUMBER: 60/049787
: PRIOR FILING DATE: 1997-06-16
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/065186
: PRIOR FILING DATE: 1997-11-12
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066770
: PRIOR FILING DATE: 1997-11-24
: PRIOR APPLICATION NUMBER: 60/075945
: PRIOR FILING DATE: 1998-02-25
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/083322
: PRIOR FILING DATE: 1998-04-28
: PRIOR APPLICATION NUMBER: 60/084600
: PRIOR FILING DATE: 1998-05-07
: PRIOR APPLICATION NUMBER: 60/087106
: PRIOR FILING DATE: 1998-05-28
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 532
: SEQ ID NO 295
: LENGTH: 237
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-992-643-295

Query Match
Best Local Similarity 76.9%; Score 30; DB 5; Length 237;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXPCXC 10
      | | |
Db 122 NAECPAC 128

RESULT 4
: Sequence 222, Application US/10125923A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Chen, Jian
: APPLICANT: Desnoyers, Luc
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Pan, James
: APPLICANT: Smith, Victoria
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3430R1C79
: CURRENT APPLICATION NUMBER: US/10/125,923A
: CURRENT FILING DATE: 2002-01-15
: PRIOR APPLICATION NUMBER: 10/052586
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; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 222
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-125-923A-222
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Query Match          76.9%; Score 30; DB 6; Length 237;
Best Local Similarity 57.1%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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OY 4 NXXCPXC 10
Db 122 NAECPC 128
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RESULT 5
US-10-205-892-222
; Sequence 222, Application US/10205892
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C517
; CURRENT APPLICATION NUMBER: US/10/205,892
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
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; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 222
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-205-892-222
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Query Match          76.9%; Score 30; DB 6; Length 237;
Best Local Similarity 57.1%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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OY 4 NXXCPXC 10
Db 122 NAECPC 128
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RESULT 6
US-10-174-575-222
; Sequence 222, Application US/10174575
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C35
; CURRENT APPLICATION NUMBER: US/10/174,575
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 222
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174-575-222
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Db 122 NAECPCAC 128

## RESULT 7

US-10-174-575A-222  
; Sequence 222, Application US/10174575A  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C35  
; CURRENT APPLICATION NUMBER: US/10/174,575A  
; CURRENT FILING DATE: 2002-06-18  
; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 232  
; LENGTH: 237  
; TYPE: PRT  
; ORGANISM: Homo Saplen  
US-10-174-575A-222

Query Match 76.9%; Score 30; DB 6; Length 237;  
Best Local Similarity 57.1%; Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
Db 122 NAECPCAC 128

## RESULT 8

US-09-724-676-78297  
; Sequence 78297, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 78297

; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-676-78297

Query Match 76.9%; Score 30; DB 5; Length 332;  
Best Local Similarity 57.1%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
Db 225 NRTCPTC 231

## RESULT 9

US-09-724-676-78298  
; Sequence 78298, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 78298  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-676-78298

Query Match 76.9%; Score 30; DB 5; Length 332;  
Best Local Similarity 57.1%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
Db 225 NRTCPTC 231

## RESULT 10

US-09-724-676A-78297  
; Sequence 78297, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 78297  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-676A-78297

Query Match 76.9%; Score 30; DB 5; Length 332;  
Best Local Similarity 57.1%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
Db 225 NRTCPTC 231

## RESULT 11

US-09-724-676A-78298  
; Sequence 78298, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen



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; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patentln version 3.2
; SEQ ID NO 78298
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-78298

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```

Query Match          76.9%; Score 30; DB 5; Length 332;
Best Local Similarity 57.1%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 4 NXXCPXC 10
DB 225 NHTCPTC 231

```

```

RESULT 12
US-09-724-676-78522
; Sequence 78522, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patentln version 3.2
; SEQ ID NO 78522
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-78522

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Query Match          76.9%; Score 30; DB 5; Length 550;
Best Local Similarity 57.1%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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```

QY 4 NXXCPXC 10
DB 224 NHTCPTC 230

```

```

RESULT 13
US-09-724-676A-78522
; Sequence 78522, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patentln version 3.2
; SEQ ID NO 78522
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-78522

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```

Query Match          76.9%; Score 30; DB 5; Length 550;
Best Local Similarity 57.1%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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```

QY 4 NXXCPXC 10
DB 224 NHTCPTC 230

```

```

RESULT 14
US-09-724-676-78521

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; Sequence 78521, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patentln version 3.2
; SEQ ID NO 78521
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-78521

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```

Query Match          76.9%; Score 30; DB 5; Length 555;
Best Local Similarity 57.1%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 4 NXXCPXC 10
DB 224 NHTCPTC 230

```

```

RESULT 15
US-09-724-676A-78521
; Sequence 78521, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patentln version 3.2
; SEQ ID NO 78521
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-78521

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```

Query Match          76.9%; Score 30; DB 5; Length 555;
Best Local Similarity 57.1%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 4 NXXCPXC 10
DB 224 NHTCPTC 230

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Search completed: December 13, 2002, 08:45:51
Job time: 1.91411 secs

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CLANK (USPTO)

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 13, 2002, 08:37:10 ; Search time 20.0982 Seconds  
(without alignments)  
384.951 Million cell updates/sec

Title: US-09-701-080C-1

Perfect score: 39

Sequence: 1 XXXNXXCPXCXX 12

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Searched: 4569144 seqs, 644733110 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	79.5	79	21	US-09-733-089-23902
2	31	79.5	79	22	US-09-816-660-23902
3	31	79.5	82	21	US-09-733-089-20004
4	31	79.5	82	22	US-09-816-660-20004
5	31	79.5	243	25	US-10-155-881-9389
6	31	79.5	339	25	US-10-155-881-29457

7	31	79.5	367	21	US-09-791-537-12171	Sequence 12171, A
8	31	79.5	367	21	US-09-791-537-15887	Sequence 15887, A
9	31	79.5	534	27	US-60-360-039-5906	Sequence 5906, Ap
10	31	79.5	635	19	US-09-540-236-2296	Sequence 2296, Ap
11	31	79.5	635	27	US-60-128-476-3650	Sequence 3650, Ap
12	30	76.9	19	1	PCT-US94-07194-3	Sequence 3, Appl1
13	30	76.9	61	26	US-10-219-999-51491	Sequence 51491, A
14	30	76.9	61	27	US-60-312-544-7377	Sequence 7377, A
15	30	76.9	73	17	US-09-330-781-260	Sequence 260, App
16	30	76.9	73	22	US-09-828-769-260	Sequence 260, App
17	30	76.9	75	21	US-09-708-427-58792	Sequence 58792, A
18	30	76.9	78	20	US-09-617-681A-5073	Sequence 5073, Ap
19	30	76.9	87	20	US-09-617-682A-925	Sequence 925, App
20	30	76.9	87	25	US-10-155-881-22445	Sequence 22445, A
21	30	76.9	88	21	US-09-733-089-15530	Sequence 15530, A
22	30	76.9	88	22	US-09-816-660-15530	Sequence 15530, A
23	30	76.9	93	21	US-09-708-427-58791	Sequence 58791, A
24	30	76.9	96	22	US-09-733-089-5237	Sequence 5237, Ap
25	30	76.9	96	22	US-09-816-660-5237	Sequence 5237, Ap
26	30	76.9	100	21	US-09-708-427-58790	Sequence 58790, A
27	30	76.9	100	25	US-10-155-881-34015	Sequence 34015, A
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29	30	76.9	100	27	US-60-324-109-20832	Sequence 20832, A
30	30	76.9	101	23	US-09-902-540-16156	Sequence 16156, A
31	30	76.9	104	20	US-09-617-681A-5072	Sequence 5072, Ap
32	30	76.9	104	21	US-09-733-089-5145	Sequence 5145, Ap
33	30	76.9	104	22	US-09-816-660-5145	Sequence 5145, Ap
34	30	76.9	104	25	US-10-155-881-22620	Sequence 22620, A
35	30	76.9	110	25	US-10-155-881-34028	Sequence 34028, A
36	30	76.9	113	20	US-09-617-682A-924	Sequence 924, App
37	30	76.9	115	25	US-10-155-881-15442	Sequence 15442, A
38	30	76.9	115	27	US-60-312-544-6368	Sequence 6368, Ap
39	30	76.9	116	19	PCT-US01-04098A-3697	Sequence 6324, Ap
40	30	76.9	118	1	PCT-US01-04098A-3697	Sequence 3697, Ap
41	30	76.9	119	21	US-09-708-427-58791	Sequence 58791, A
42	30	76.9	120	21	US-09-733-089-15442	Sequence 15442, A
43	30	76.9	120	22	US-09-816-660-15442	Sequence 15442, A
44	30	76.9	122	25	US-10-155-881-33987	Sequence 33987, A
45	30	76.9	122	27	US-60-312-544-5588	Sequence 5588, Ap

#### ALIGNMENTS

RESULT 1

US-09-733-089-23902

; Sequence 23902, Application US/09733089

; GENERAL INFORMATION:

; APPLICANT: Dotson, Stanton B.

; APPLICANT: Kovacic, David K.

; APPLICANT: Liu, Jingdong

; APPLICANT: Lufiyya, Linda L.

; APPLICANT: McIninch, James

; APPLICANT: Wu, Wei

; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With

; FILE REFERENCE: 38-21(15300)D

; CURRENT APPLICATION NUMBER: US/09/733,089

; PRIOR FILING DATE: 2000-12-11

; PRIOR APPLICATION NUMBER: US 09/474,435

; PRIOR FILING DATE: 1999-12-28

; PRIOR APPLICATION NUMBER: US 09/654,617

; PRIOR FILING DATE: 2000-09-05

; PRIOR APPLICATION NUMBER: US 09/620,392

; PRIOR FILING DATE: 2000-07-19

; NUMBER OF SEQ ID NOS: 24143

; SEQ ID NO 23902

; LENGTH: 79

; TYPE: PRT

; ORGANISM: Oryza sativa

US-09-733-089-23902

Query Match 79.5%; Score 31; DB 21; Length 79;

Best Local Similarity 57.1%; Pred. No. 1.9e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPC 10  
| | | |  
Db 31 NSSCPSC 37

RESULT 2  
US-09-816-660-23902

; Sequence 23902, Application US/09816660  
; GENERAL INFORMATION:  
; APPLICANT: Dotson, Stanton B.  
; APPLICANT: Kovall, David K.  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Lutfiyya, Linda L.  
; APPLICANT: McIninch, James  
; APPLICANT: Wu, Wei  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 38-21(15300)D  
; CURRENT APPLICATION NUMBER: US/09/816,660  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: US 09/474,435  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: US 09/654,617  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: US 09/733,089  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: ) US 09/684,016  
; PRIOR FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 09/620,392  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 24143  
; SEQ ID NO 23902  
; LENGTH: 79  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-09-816-660-23902

Query Match 79.5%; Score 31; DB 22; Length 79;  
Best Local Similarity 57.1%; Pred. No. 1.9e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPC 10  
| | | |  
Db 31 NSSCPSC 37

RESULT 3  
US-09-733-089-20004

; Sequence 20004, Application US/09733089  
; GENERAL INFORMATION:  
; APPLICANT: Dotson, Stanton B.  
; APPLICANT: Kovall, David K.  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Lutfiyya, Linda L.  
; APPLICANT: McIninch, James  
; APPLICANT: Wu, Wei  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 38-21(15300)D  
; CURRENT APPLICATION NUMBER: US/09/733,089  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 09/474,435  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: US 09/654,617  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: US 09/620,392  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 24143  
; SEQ ID NO 20004  
; LENGTH: 82  
; TYPE: PRT  
; ORGANISM: Zea mays

; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-09-733-089-20004

Query Match 79.5%; Score 31; DB 21; Length 82;  
Best Local Similarity 57.1%; Pred. No. 2e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPC 10  
| | | |  
Db 20 NSSCPSC 26

RESULT 4  
US-09-816-660-20004

; Sequence 20004, Application US/09816660  
; GENERAL INFORMATION:  
; APPLICANT: Dotson, Stanton B.  
; APPLICANT: Kovall, David K.  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Lutfiyya, Linda L.  
; APPLICANT: McIninch, James  
; APPLICANT: Wu, Wei  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 38-21(15300)D  
; CURRENT APPLICATION NUMBER: US/09/816,660  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: US 09/474,435  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: US 09/654,617  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: US 09/733,089  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: ) US 09/684,016  
; PRIOR FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 09/620,392  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 24143  
; SEQ ID NO 20004  
; LENGTH: 82  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-09-816-660-20004

Query Match 79.5%; Score 31; DB 22; Length 82;  
Best Local Similarity 57.1%; Pred. No. 2e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPC 10  
| | | |  
Db 20 NSSCPSC 26

RESULT 5  
US-10-155-881-9389

; Sequence 9389, Application US/10155881  
; GENERAL INFORMATION:  
; APPLICANT: Dotson, Stanton B.  
; APPLICANT: Kovall, David K.  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Lutfiyya, Linda L.  
; APPLICANT: McIninch, James  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; FILE REFERENCE: 38-21(15300)J  
; CURRENT APPLICATION NUMBER: US/10/155,881  
; PRIOR FILING DATE: 2002-05-22  
; NUMBER OF SEQ ID NOS: 37595  
; SEQ ID NO 9389  
; LENGTH: 243  
; TYPE: PRT  
; ORGANISM: Zea mays

Fri Dec 13 09:02:56 2002

US-10-155-881-9389

Query Match  
Best Local Similarity 79.5%; Score 31; DB 25; Length 243;  
Pred. No. 4.1e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
| | | |  
Db 23 NASCPSC 29

RESULT 6  
US-10-155-881-29457

; Sequence 29457, Application US/10155881

; GENERAL INFORMATION:

; APPLICANT: Dotson, Stanton B.

; APPLICANT: Kovalic, David K.

; APPLICANT: Liu, Jingdong

; APPLICANT: Lutfiyya, Linda L.

; APPLICANT: McIninch, James

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH

; FILE REFERENCE: 38-21(15300)J

; CURRENT APPLICATION NUMBER: US/10/155,881

; CURRENT FILING DATE: 2002-05-22

; NUMBER OF SEQ ID NOS: 37595

; SEQ ID NO 29457

; LENGTH: 339

; TYPE: PRT

; ORGANISM: Oryza sativa

US-10-155-881-29457

Query Match  
Best Local Similarity 79.5%; Score 31; DB 25; Length 339;  
Pred. No. 5.1e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
| | | |  
Db 277 NSSCPSC 283

RESULT 7  
US-09-791-537-12171

; Sequence 12171, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Blonoxix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 12171

; LENGTH: 367

; TYPE: PRT

; ORGANISM: Pyrococcus abyssi

US-09-791-537-12171

Query Match  
Best Local Similarity 79.5%; Score 31; DB 21; Length 367;  
Pred. No. 5.3e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
| | | |  
Db 240 NTTCPTC 246

RESULT 8  
US-09-791-537-15887  
; Sequence 15887, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Blonoxix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 15887

; LENGTH: 367

; TYPE: PRT

; ORGANISM: Pyrococcus furiosus

US-09-791-537-15887

Query Match  
Best Local Similarity 79.5%; Score 31; DB 21; Length 367;  
Pred. No. 5.3e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
| | | |  
Db 240 NTTCPTC 246

RESULT 9  
US-60-360-039-5906

; Sequence 5906, Application US/60360039

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Chen, Xianfeng

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)A

; CURRENT APPLICATION NUMBER: US/60/360,039

; CURRENT FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 5906

; LENGTH: 534

; TYPE: PRT

; ORGANISM: Caenorhabditis elegans

US-60-360-039-5906

Query Match  
Best Local Similarity 79.5%; Score 31; DB 27; Length 534;  
Pred. No. 6.8e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
| | | |  
Db 135 NASCPSC 141

RESULT 10  
US-09-540-236-2296

; Sequence 2296, Application US/09540236

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CA

; FILE REFERENCE: 2709.2005-001

; CURRENT APPLICATION NUMBER: US/09/540,236

; CURRENT FILING DATE: 2000-04-04

; NUMBER OF SEQ ID NOS: 3840

; SEQ ID NO 2296

; LENGTH: 635

; TYPE: PRT

; ORGANISM: M. catarrhalis

US-09-540-236-2296

Query Match 79.5%; Score 31; DB 19; Length 635;  
Best Local Similarity 57.1%; Pred. No. 7.6e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
| | | |  
Db 206 NSACPTC 212

RESULT 11  
US-60-128-476-3650  
; Sequence 3650, Application US/60128476  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Bretton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA  
; FILE REFERENCE: 107196.139  
; CURRENT APPLICATION NUMBER: US/60/128,476  
; CURRENT FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 5002  
; SEQ ID NO 3650  
; LENGTH: 635  
; TYPE: PRT  
; ORGANISM: Moraxella catarrhalis  
US-60-128-476-3650

Query Match 79.5%; Score 31; DB 27; Length 635;  
Best Local Similarity 57.1%; Pred. No. 7.6e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
| | | |  
Db 206 NSACPTC 212

RESULT 12  
PCT-US94-07194-3  
; Sequence 3, Application PC/TUS9407194  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: CONOTOXINS I  
; NUMBER OF SEQUENCES: 13  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/07194  
; FILING DATE: 27-JUN-1994  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/084,848  
; FILING DATE: June 29, 1993  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
PCT-US94-07194-3

Query Match 76.9%; Score 30; DB 1; Length 19;  
Best Local Similarity 71.4%; Pred. No. 1.1e+03;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
| | | |  
Db 6 NAACPXC 12

RESULT 13  
US-10-219-999-51491

; Sequence 51491, Application US/10219999  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Edgerton, Michael D  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Liu, Jindong  
; APPLICANT: Stein, Joshua  
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-10(52726)C  
; CURRENT APPLICATION NUMBER: US/10/219,999  
; CURRENT FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: US 60/324,109  
; PRIOR FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: US 60/312,544  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 63520  
; SEQ ID NO 51491  
; LENGTH: 61  
; TYPE: PRT  
; ORGANISM: Zea mays  
US-10-219-999-51491

Query Match 76.9%; Score 30; DB 26; Length 61;  
Best Local Similarity 57.1%; Pred. No. 2.3e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
| | | |  
Db 46 NATCPLC 52

RESULT 14  
US-60-312-544-7377  
; Sequence 7377, Application US/60312544  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Edgerton, Michael D  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Liu, Jindong  
; APPLICANT: Stein, Joshua  
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-10(52726)A  
; CURRENT APPLICATION NUMBER: US/60/312,544  
; CURRENT FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 10730  
; SEQ ID NO 7377  
; LENGTH: 61  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 701125331\_FLI  
US-60-312-544-7377

Query Match 76.9%; Score 30; DB 27; Length 61;  
Best Local Similarity 57.1%; Pred. No. 2.3e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
| | | |  
Db 36 NSTCPLC 42

RESULT 15  
US-09-330-781-260  
; Sequence 260, Application US/09330781  
; GENERAL INFORMATION:  
; APPLICANT: Geating, David P.  
; APPLICANT: Robison, Keith E.  
; APPLICANT: Holtzman, Douglas A.  
; TITLE OF INVENTION: Nucleic Acid Molecules Derived from a  
; TITLE OF INVENTION: Human Prostate Stromal Cell Library

Fri Dec 13 09:02:56 2002

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: FILE REFERENCE: MLN98-26DA
: CURRENT APPLICATION NUMBER: US/09/330,781
: CURRENT FILING DATE: 1999-06-11
: PRIOR APPLICATION NUMBER: 60/090,179
: PRIOR FILING DATE: 1998-06-22
: NUMBER OF SEQ ID NOS: 490
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO: 260
: LENGTH: 73
: TYPE: PRF
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SIGNAL
: LOCATION: (1)...(23)
US-09-330-781-260
    
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Query Match          76.9%; Score 30; DB 17; Length 73;
Best Local Similarity 57.1%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
    
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QY 4 NXXCPYC 10
DB 49 NSOCPAC 55
    
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Search completed: December 13, 2002, 08:44:49  
 Job time: 22.0982 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 13, 2002, 08:39:46 : Search time 1.17791 Seconds  
(without alignments)  
169.748 Million cell updates/sec

Title: US-09-701-080C-1  
Perfect score: 39  
Sequence: 1 XXXNXXCPXCXX 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105981 seqs, 16662342 residues

Total number of hits satisfying chosen parameters: 105981

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published\_Applications\_AA.\*  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
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12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
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14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	76.9	147	10	US-09-764-864-1289
2	30	76.9	199	10	US-09-764-864-1291
3	30	76.9	201	10	US-09-764-864-836
4	30	76.9	237	9	US-09-992-598-295
5	30	76.9	237	9	US-09-989-295A-295
6	30	76.9	237	10	US-09-989-722-295
7	30	76.9	237	10	US-09-989-723-295
8	30	76.9	237	10	US-09-989-279-295
9	30	76.9	237	10	US-09-989-727-295
10	30	76.9	237	10	US-09-989-731-295
11	30	76.9	237	10	US-09-989-732-295
12	30	76.9	237	10	US-09-991-073-295
13	30	76.9	237	10	US-09-991-163-295
14	30	76.9	237	10	US-09-993-604-295
15	30	76.9	237	10	US-09-990-456-295
16	30	76.9	237	10	US-09-989-721-295
17	30	76.9	237	12	US-10-052-586-222
18	30	76.9	266	10	US-09-764-864-834
19	30	76.9	266	10	US-09-764-864-834

20	30	76.9	718	10	US-09-823-635-2	Sequence 2, Appli
21	30	76.9	810	10	US-09-976-165-34	Sequence 34, Appli
22	30	76.9	816	10	US-09-976-165-37	Sequence 37, Appli
23	29	74.4	149	10	US-09-804-969-8	Sequence 8, Appli
24	29	74.4	164	10	US-09-925-301-1278	Sequence 1278, Ap
25	29	74.4	239	10	US-09-804-969-2	Sequence 2, Appli
26	29	74.4	239	10	US-09-804-969-10	Sequence 10, Appli
27	29	74.4	261	10	US-09-804-969-12	Sequence 12, Appli
28	29	74.4	329	10	US-09-804-969-4	Sequence 4, Appli
29	29	74.4	336	9	US-09-991-888-2	Sequence 2, Appli
30	29	74.4	351	10	US-09-804-969-6	Sequence 6, Appli
31	29	74.4	580	10	US-09-925-301-943	Sequence 943, App
32	29	74.4	642	9	US-10-145-949A-8	Sequence 8, Appli
33	29	74.4	647	9	US-10-145-949A-6	Sequence 6, Appli
34	29	74.4	679	9	US-10-145-949A-4	Sequence 4, Appli
35	29	74.4	684	9	US-10-145-949A-2	Sequence 2, Appli
36	29	74.4	710	10	US-09-815-242-5367	Sequence 5367, Ap
37	29	74.4	711	10	US-09-815-242-12190	Sequence 12190, A
38	29	74.4	940	10	US-09-805-242-10447	Sequence 10447, A
39	29	74.4	943	10	US-09-815-242-10994	Sequence 10994, A
40	29	74.4	1065	10	US-09-900-237-33	Sequence 33, Appli
41	28	71.8	106	10	US-09-764-864-1478	Sequence 1478, Ap
42	28	71.8	113	10	US-09-826-312-8	Sequence 8, Appli
43	28	71.8	118	10	US-09-764-864-826	Sequence 826, App
44	28	71.8	131	10	US-09-764-864-1285	Sequence 1285, Ap
45	28	71.8	404	10	US-09-764-864-1055	Sequence 1055, Ap

#### ALIGNMENTS

RESULT 1  
US-09-764-864-1289  
; Sequence 1289, Application US/09764864  
; Patent No. US20020132753A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT223  
; CURRENT APPLICATION NUMBER: US/09/764, 864  
; PRIORITY FILING DATE: 2001-01-17  
; Prior application data removed - consult PAM or file wrapper  
; NUMBER OF SEQ ID NOS: 1792  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1289  
; LENGTH: 147  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (95)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (128)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (147)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-764-864-1289

Query Match  
Best local Similarity 76.9%; Score 30; DB 10; Length 147;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
DB 27 NSQCPC 33

RESULT 2  
US-09-764-864-1291  
; Sequence 1291, Application US/09764864  
; Patent No. US20020132753A1

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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; PRIORITY FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1291
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (187)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1291

Query Match
Best Local Similarity 76.9%; Score 30; DB 10; Length 199;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXCPXC 10
Db 179 NSTCPIC 185

RESULT 3
US-09-764-864-836
; Sequence 836, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; PRIORITY FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 836
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-836

Query Match
Best Local Similarity 76.9%; Score 30; DB 10; Length 201;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXCPXC 10
Db 181 NSTCPIC 187

RESULT 4
US-09-992-598-295
; Sequence 295, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
```

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; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; PRIORITY FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 60/049787
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1291
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (187)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1291

Query Match
Best Local Similarity 76.9%; Score 30; DB 10; Length 199;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXCPXC 10
Db 179 NSTCPIC 185

RESULT 3
US-09-764-864-836
; Sequence 836, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; PRIORITY FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 836
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-836

Query Match
Best Local Similarity 76.9%; Score 30; DB 10; Length 201;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXCPXC 10
Db 181 NSTCPIC 187

RESULT 4
US-09-992-598-295
; Sequence 295, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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PRIOR FILING DATE: 1998-06-10  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 76.9%; Score 30; DB 9; Length 237;  
Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
Db 122 NAECPAC 128

RESULT 5  
US-09-989-293A-295  
Sequence 295, Application US/09989293A  
Patent No. US20020177164A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bostein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C66  
CURRENT APPLICATION NUMBER: US/09/989,293A  
PRIOR FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
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;; PRIOR FILING DATE: 1998-07-09

Query Match 76.9%; Score 30; DB 9; Length 237;  
Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 122 NACPCAC 128

RESULT 6  
US-09-989-722-295  
; Sequence 295, Application US/09989722  
; Patent No. US20020072067A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gertschen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gueney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Raoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same

;; FILE REFERENCE: P2730PIC63  
;; CURRENT APPLICATION NUMBER: US/09/989,722  
;; CURRENT FILING DATE: 2001-11-19  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
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;; PRIOR APPLICATION NUMBER: 60/090540  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090542  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090557  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090676  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090678  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090690  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090694  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090695

;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090696  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090862  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/090863  
;; PRIOR FILING DATE: 1998-06-26  
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;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 76.9%; Score 30; DB 10; Length 237;  
Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
I I I  
Db 122 NAECPCAC 128

RESULT 7  
US-09-989-723-295  
; Sequence 295, Application US/09989723  
; Patent No. US20020072092A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Bolstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Geriltsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PLC62  
; CURRENT APPLICATION NUMBER: US/09/989,723  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17



;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

## Query Match

76.9%; Score 30; DB 10; Length 237;

Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXCPXC 10  
1 11 1  
Db 122 NAECPAC 128

## RESULT 8

US-09-989-279-295

; Sequence 295, Application US/09989279

; Patent No. US20020072496A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerltsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kijavlin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paonli, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730PIC56

; CURRENT APPLICATION NUMBER: US/09/989, 279

; CURRENT FILING DATE: 2001-11-19

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 60/075945

; PRIOR FILING DATE: 1998-02-25

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/083322

; PRIOR FILING DATE: 1998-04-28

; PRIOR APPLICATION NUMBER: 60/084600

; PRIOR FILING DATE: 1998-05-07

; PRIOR APPLICATION NUMBER: 60/087106

; PRIOR FILING DATE: 1998-05-28

; PRIOR APPLICATION NUMBER: 60/087607

; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: 60/087609

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; PRIOR APPLICATION NUMBER: 60/087827

; PRIOR FILING DATE: 1998-06-03

; PRIOR APPLICATION NUMBER: 60/088021

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; PRIOR FILING DATE: 1998-06-04

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; PRIOR FILING DATE: 1998-06-04

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; PRIOR FILING DATE: 1998-06-17



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 PRIOR APPLICATION NUMBER: 60/090863  
 PRIOR FILING DATE: 1998-06-26  
 PRIOR APPLICATION NUMBER: 60/091360  
 PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091478  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091544  
 PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091519

PRIOR FILING DATE: 1998-07-02  
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 PRIOR FILING DATE: 1998-07-02  
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 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091978  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match 76.9%; Score 30; DB 10; Length 237;  
 Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
 Db 122 NAECPAC 128

RESULT 9  
 US-09-989-727-295  
 Sequence 295, Application US/09989727  
 Patent No. US20020072497A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C65  
 CURRENT APPLICATION NUMBER: US/09/989,727  
 CURRENT FILING DATE: 2001-11-19  
 PRIOR APPLICATION NUMBER: 60/049787  
 PRIOR FILING DATE: 1997-06-16  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/065186  
 PRIOR FILING DATE: 1997-11-12  
 PRIOR APPLICATION NUMBER: 60/065311  
 PRIOR FILING DATE: 1997-11-13  
 PRIOR APPLICATION NUMBER: 60/066770  
 PRIOR FILING DATE: 1997-11-24  
 PRIOR APPLICATION NUMBER: 60/075945  
 PRIOR FILING DATE: 1998-02-25  
 PRIOR APPLICATION NUMBER: 60/078910  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/083322  
 PRIOR FILING DATE: 1998-04-28  
 PRIOR APPLICATION NUMBER: 60/084600  
 PRIOR FILING DATE: 1998-05-07



PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 76.9%; Score 30; DB 10; Length 237;  
Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
DB 122 NAECPAC 128

RESULT 10  
US-09-989-731-295  
Sequence 295, Application US/09989731  
Patent No. US20020103125A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C70  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083332  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759

PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088026  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088028  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
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PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088167  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088202  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088212  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088217  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088655  
PRIOR FILING DATE: 1998-06-09  
PRIOR APPLICATION NUMBER: 60/088734  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088738  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/08742  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088810  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
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PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088876  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089440  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089512  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089598  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089600  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089908  
PRIOR FILING DATE: 1998-06-18



;; PRIOR APPLICATION NUMBER: 60/088026  
;; PRIOR FILING DATE: 1998-06-04  
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;; PRIOR FILING DATE: 1998-06-04  
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;; PRIOR FILING DATE: 1998-06-04  
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;; PRIOR FILING DATE: 1998-06-04  
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Query Match 76.9%; Score 30; DB 10; Length 237;  
Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
DB 122 NACCPAC 128

RESULT 12  
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 ; Sequence 295, Application US/09991073  
 ; Patent No. US2002012756A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
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 ; APPLICANT: Goddard, Audrey  
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 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2730PIC15  
 ; CURRENT APPLICATION NUMBER: US/09/991,073  
 ; PRIOR FILING DATE: 2001-11-14  
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Query Match 76.9%; Score 30; DB 10; Length 237;  
Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.

;; APPLICANT: Botstein, David  
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;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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Query Match 76.9% Score 30; DB 10; Length 237;  
Best Local Similarity 57.1% Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
Db 122 MACCPAC 128

RESULT 14  
US-09-991-163-295  
Sequence 295, Application US/09991163  
Patent No. US20020132253A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.



APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
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APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC17  
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? PRIOR FILING DATE: 1998-07-09

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Query Match 76.9%; Score 30; DB 10; Length 237;
Best Local Similarity 57.1%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 4 NXCPXC 10
Db 122 NAECFAC 128

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RESULT 15
US-09-993-604-295
Sequence 295, Application US/09993604
Patent No. US20020137075A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geriltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James

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? APPLICANT: Paoni, Nicholas F.
? APPLICANT: Roy, Margaret Ann
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tumas, Daniel
? APPLICANT: Watanabe, Colin K.
? APPLICANT: Williams, P. Mickey
? APPLICANT: Wood, William I.
? APPLICANT: Zhang, Zemin
? TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
? Acids Encoding the Same
? FILE REFERENCE: P2730PIC25
? CURRENT APPLICATION NUMBER: US/09/993,604
? CURRENT FILING DATE: 2001-11-14
? PRIOR APPLICATION NUMBER: 60/049787
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Query Match 76.9% Score 30; DB 10; Length 237;  
 Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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 Db 122 NMECPAC 128

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Gencore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 13, 2002, 08:38:20 : Search time 1.69325 Seconds  
(Without alignments)  
208.519 Million cell updates/sec

Title: US-09-701-080C-1  
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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

SUMMARIES

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34	29	74.4	46	1	US-08-331-394-11	Sequence 11, Appl
35	29	74.4	46	1	US-08-250-858-11	Sequence 11, Appl
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37	29	74.4	46	2	US-08-744-139-11	Sequence 11, Appl
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ALIGNMENTS

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; Sequence 3, Application US/0804848A
; Patent No. 5432155
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Rivier, Jean E. F.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Abogadie, Fe
; APPLICANT: Hopkins, Chris E.
; APPLICANT: Dykert, John
; APPLICANT: Torres, Josep L.
; TITLE OF INVENTION: Conotoxins I
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitch, Even, Tabin & Flannery
; STREET: 135 South LaSalle Street, Suite 900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/084,848A
; FILING DATE: June 29, 1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Schumann, James J.
; REGISTRATION NUMBER: 20856
; REFERENCE/DOCKET NUMBER: 52511
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)552-1311
; TELEFAX: (619)552-0095
; TELEX: 20 6566 PATIWA CGO
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-084-848A-3
;
Query Match      76.9%; Score 30; DB 1; Length 19;
Best Local Similarity 71.4%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 6 NAACPXC 12

## RESULT 2

US-08-458-499-3  
Sequence 3, Application US/08458499  
Patent No. 5700778  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Rivier, Jean E. F.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Abogadie, Fe  
APPLICANT: Hopkins, Chris E.  
APPLICANT: Dykert, John  
APPLICANT: Torres, Josep L.  
TITLE OF INVENTION: Conotoxins I  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitch, Even, Tabin & Flannery  
STREET: 135 South LaSalle Street, Suite 900  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,499  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/084,848  
FILING DATE: June 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Schumann, James J.  
REGISTRATION NUMBER: 20856  
REFERENCE/DOCKET NUMBER: 52511  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)552-1311  
TELEFAX: (619)552-0095  
TELEX: 20 6566 PATLAW CGO  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-458-499-3

Query Match 76.9%; Score 30; DB 1; Length 19;  
Best Local Similarity 71.4%; Pred. No. 37;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
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## RESULT 3

US-09-227-357-154  
Sequence 154, Application US/09227357  
Patent No. 6342581  
GENERAL INFORMATION:  
APPLICANT: Filscher et al.  
TITLE OF INVENTION: 123 Human Secreted Proteins  
FILE REFERENCE: P2010P1  
CURRENT APPLICATION NUMBER: US/09/227,357  
CURRENT FILING DATE: 1999-01-08

EARLIER APPLICATION NUMBER: PCT/US98/13684  
EARLIER FILING DATE: 1998-07-07  
EARLIER APPLICATION NUMBER: 60/051,926  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,793  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,925  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,929  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,803  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,732  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,931  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,932  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,916  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,930  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,918  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,920  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,733  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,795  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,919  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,928  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/055,722  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,723  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,948  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,949  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,953  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,950  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,947  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,964  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/056,360  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,684  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,984  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,954  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/058,785  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,664  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,660  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,661  
EARLIER FILING DATE: 1997-09-12  
NUMBER OF SEQ ID NOS: 672  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 154  
LENGTH: 237  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:

NAME/KEY: SITE  
LOCATION: (137)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (151)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-227-357-154

Query Match 76.9%; Score 30; DB 4; Length 237;  
Best Local Similarity 57.1%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
1 1 1 1  
DB 122 NACCPAC 128

## RESULT 4

US-08-560-398-12  
Sequence 12, Application US/08560398  
Patent No. 5907082

GENERAL INFORMATION:  
APPLICANT: O'Neill, Sharmen  
ATTORNEY/AGENT INFORMATION:  
TITLE OF INVENTION: Ovule-Specific Gene Expression  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/560,398  
FILING DATE: 17-NOV-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 023070-0633000US

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 718 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-560-398-12

Query Match 76.9%; Score 30; DB 2; Length 718;  
Best Local Similarity 57.1%; Pred. No. 4.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
1 1 1 1  
DB 105 NACCPAC 111

## RESULT 5

US-08-560-398-2  
Sequence 2, Application US/08560398  
Patent No. 5907082

GENERAL INFORMATION:  
APPLICANT: O'Neill, Sharmen

APPLICANT: Nadeau, Jeanette  
TITLE OF INVENTION: Ovule-Specific Gene Expression  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/560,398  
FILING DATE: 17-NOV-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 023070-0633000US

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 768 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-560-398-2

Query Match 76.9%; Score 30; DB 2; Length 768;  
Best Local Similarity 57.1%; Pred. No. 5.2e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
1 1 1 1  
DB 176 NACCPAC 182

## RESULT 6

US-08-820-170A-34  
Sequence 34, Application US/08820170A  
Patent No. 5831058

GENERAL INFORMATION:  
APPLICANT: Tsutomu, FUJIMARA  
ATTORNEY/AGENT INFORMATION:  
APPLICANT: Masato, HORIE  
APPLICANT: Toyomasa, KATAGIRI  
TITLE OF INVENTION: HUMAN GENE  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Sughrue, Mion, Zinn, Macpeak & Seas  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States  
ZIP: 20037-3202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/820,170A  
FILING DATE:  
CLASSIFICATION: 536  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 293-7060  
TELEFAX: (202) 293-7860

TELEX: 6491103  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 810 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-820-170A-34

Query Match 76.9%; Score 30; DB 2; Length 810;  
Best Local Similarity 57.1%; Pred. No. 5.4e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPCX 10  
| | |  
Db 224 NHTCPTC 230

RESULT 7  
US-09-055-699-34  
; Sequence 34, Application US/09055699  
; Patent No. 6005088

GENERAL INFORMATION:  
; APPLICANT: Tsutomu, FUJIMURA  
; APPLICANT: Takeshi, WATANABE  
; APPLICANT: Masato, HORIE  
; APPLICANT: Toyomasa, KATAGIRI  
; TITLE OF INVENTION: HUMAN GENE  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Sugitue, Mion, Zinn, Macpeak & Seas  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: United States  
; ZIP: 20037-3202

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/055,699

CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/820,170

FILING DATE:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 293-7060  
; TELEFAX: (202) 293-7860  
; TELEX: 6491103  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 810 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-055-699-34

Query Match 76.9%; Score 30; DB 3; Length 810;  
Best Local Similarity 57.1%; Pred. No. 5.4e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPCX 10  
| | |  
Db 224 NHTCPTC 230

RESULT 8  
US-09-273-565-34  
; Sequence 34, Application US/09273565A  
; Patent No. 6166190

GENERAL INFORMATION:  
; APPLICANT: FUJIMURA, TSUTOMU  
; APPLICANT: WATANABE, TAKESHI  
; APPLICANT: HORIE, MASATO  
; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN  
; SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME  
; FILE REFERENCE: Q-53599  
; CURRENT APPLICATION NUMBER: US/09/273,565A  
; CURRENT FILING DATE: 1999-03-22  
; EARLIER APPLICATION NUMBER: 09/055,699  
; EARLIER FILING DATE: 1998-04-07  
; EARLIER APPLICATION NUMBER: 08/820,170  
; EARLIER FILING DATE: 1997-03-19  
; EARLIER APPLICATION NUMBER: JP 63410/1996  
; EARLIER FILING DATE: 1996-03-19  
; EARLIER APPLICATION NUMBER: JP 69163/1997  
; EARLIER FILING DATE: 1997-03-05  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 810  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-273-565-34

Query Match 76.9%; Score 30; DB 4; Length 810;  
Best Local Similarity 57.1%; Pred. No. 5.4e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPCX 10  
| | |  
Db 224 NHTCPTC 230

RESULT 9  
US-09-565-538-34  
; Sequence 34, Application US/09565538  
; Patent No. 6333404

GENERAL INFORMATION:  
; APPLICANT: FUJIMURA, TSUTOMU  
; APPLICANT: WATANABE, TAKESHI  
; APPLICANT: HORIE, MASATO  
; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN  
; SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME  
; FILE REFERENCE: Q-53599  
; CURRENT APPLICATION NUMBER: US/09/565,538  
; CURRENT FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: 09/273,565  
; PRIOR FILING DATE: 1999-03-22  
; PRIOR APPLICATION NUMBER: 09/055,699  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: 08/820,170  
; PRIOR FILING DATE: 1997-03-19  
; PRIOR APPLICATION NUMBER: JP 63410/1996  
; PRIOR FILING DATE: 1996-03-19  
; PRIOR APPLICATION NUMBER: JP 69163/1997  
; PRIOR FILING DATE: 1997-03-05  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 810  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-565-538-34

Query Match 76.9%; Score 30; DB 4; Length 810;  
Best Local Similarity 57.1%; Pred. No. 5.4e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPCX 10  
| | |  
Db 224 NHTCPTC 230



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RESULT 10
US-09-661-468-34
; Sequence 34, Application US/09661468
; Patent No. 6376189
; GENERAL INFORMATION:
; APPLICANT: FUJIWARA, TSUTOMU
; APPLICANT: WATANABE, TAKESHI
; APPLICANT: HORIE, MASATO
; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
; TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
; FILE REFERENCE: 0-53599
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 09/055,699
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 08/820,170
; PRIOR FILING DATE: 1997-03-19
; PRIOR APPLICATION NUMBER: JP 63410/1996
; PRIOR FILING DATE: 1996-03-19
; PRIOR APPLICATION NUMBER: JP 69163/1997
; PRIOR FILING DATE: 1997-03-05
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 810
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-661-468-34

Query Match          76.9%; Score 30; DB 4; Length 810;
Best Local Similarity 57.1%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10
DB 224 NRTCPYC 230

RESULT 11
US-08-820-170A-37
; Sequence 37, Application US/08820170A
; Patent No. 5831058
; GENERAL INFORMATION:
; APPLICANT: Tsutomu, FUJIWARA
; APPLICANT: Takeshi, WATANABE
; APPLICANT: Masato, HORIE
; APPLICANT: Toyomasa, KATAGIRI
; TITLE OF INVENTION: HUMAN GENE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/820,170A
; FILING DATE:
; CLASSIFICATION: 536
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 816 amino acids
```

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-820-170A-37

Query Match          76.9%; Score 30; DB 2; Length 816;
Best Local Similarity 57.1%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10
DB 225 NRTCPYC 231

RESULT 12
US-09-055-699-37
; Sequence 37, Application US/09055699
; Patent No. 6005088
; GENERAL INFORMATION:
; APPLICANT: Tsutomu, FUJIWARA
; APPLICANT: Takeshi, WATANABE
; APPLICANT: Masato, HORIE
; APPLICANT: Toyomasa, KATAGIRI
; TITLE OF INVENTION: HUMAN GENE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/055,699
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/820,170
; FILING DATE:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 816 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-055-699-37

Query Match          76.9%; Score 30; DB 3; Length 816;
Best Local Similarity 57.1%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10
DB 225 NRTCPYC 231

RESULT 13
US-09-273-565-37
; Sequence 37, Application US/09273565A
; Patent No. 6166190
; GENERAL INFORMATION:
; APPLICANT: FUJIWARA, TSUTOMU
; APPLICANT: WATANABE, TAKESHI
; APPLICANT: HORIE, MASATO
```

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; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
; FILE REFERENCE: O-53599
; CURRENT APPLICATION NUMBER: US/09/273,565A
; EARLIER APPLICATION NUMBER: 09/055,699
; EARLIER FILING DATE: 1998-04-07
; EARLIER APPLICATION NUMBER: 08/820,170
; EARLIER FILING DATE: 1997-03-19
; EARLIER APPLICATION NUMBER: JP 63410/1996
; EARLIER FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: JP 69163/1997
; EARLIER FILING DATE: 1997-03-05
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 37
; LENGTH: 816
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-273-565-37
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Query Match          76.9%: Score 30; DB 4; Length 816;
Best Local Similarity 57.1%: Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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OY      4  NXXCPCX 10
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Db      225 NRTCPTC 231
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RESULT 14
US-09-565-538-37
; Sequence 37, Application US/09565538
; Patent No. 6333404
; GENERAL INFORMATION:
; APPLICANT: FUJIMURA, TSUTOMU
; APPLICANT: MATANABE, TAKESHI
; APPLICANT: HORIE, MASATO
; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
; FILE REFERENCE: O-53599
; CURRENT APPLICATION NUMBER: US/09/565,538
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 09/273,565
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 09/055,699
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 08/820,170
; PRIOR FILING DATE: 1997-03-19
; PRIOR APPLICATION NUMBER: JP 63410/1996
; PRIOR FILING DATE: 1996-03-19
; PRIOR APPLICATION NUMBER: JP 69163/1997
; PRIOR FILING DATE: 1997-03-05
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 37
; LENGTH: 816
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-538-37
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Query Match          76.9%: Score 30; DB 4; Length 816;
Best Local Similarity 57.1%: Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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OY      4  NXXCPCX 10
      |  |  |
Db      225 NRTCPTC 231
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RESULT 15
US-09-661-468-37
; Sequence 37, Application US/09661468
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; Patent No. 6376189
; GENERAL INFORMATION:
; APPLICANT: FUJIMURA, TSUTOMU
; APPLICANT: MATANABE, TAKESHI
; APPLICANT: HORIE, MASATO
; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
; FILE REFERENCE: O-53599
; CURRENT APPLICATION NUMBER: US/09/661,468
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 09/055,699
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 08/820,170
; PRIOR FILING DATE: 1997-03-19
; PRIOR APPLICATION NUMBER: JP 63410/1996
; PRIOR FILING DATE: 1996-03-19
; PRIOR APPLICATION NUMBER: JP 69163/1997
; PRIOR FILING DATE: 1997-03-05
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 37
; LENGTH: 816
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-661-468-37
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Query Match          76.9%: Score 30; DB 4; Length 816;
Best Local Similarity 57.1%: Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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OY      4  NXXCPCX 10
      |  |  |
Db      225 NRTCPTC 231
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Search completed: December 13, 2002, 08:45:19
Job time : 3.69325 secs
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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 13, 2002, 08:31:04 ; Search time 4.63804 Seconds

(without alignments)  
344.760 Million cell updates/sec

Title: US-09-701-080C-1

Perfect score: 39

Sequence: 1 XXXNXXCPXCXX 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
A.GeneSeq\_101002:\*  
1: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1980.DAT:\*  
2: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1981.DAT:\*  
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4: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1983.DAT:\*  
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16: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1995.DAT:\*  
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22: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT:\*  
23: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	79.5	80	23	ABP01599
2	30	76.9	84	21	AA030183
3	30	76.9	118	22	AA080051
4	30	76.9	130	20	AA36293
5	30	76.9	136	22	AA087620
6	30	76.9	147	22	AA016336
7	30	76.9	179	21	AA036278
8	30	76.9	199	22	AA016338
9	30	76.9	200	23	AA072391
10	30	76.9	201	22	AA015883

11	30	76.9	231	22	AA025880	Human protein sequ
12	30	76.9	237	20	AA02654	Human secreted pro
13	30	76.9	237	21	AA087321	Human signal pepti
14	30	76.9	237	21	AA066721	Membrane bound pro
15	30	76.9	237	22	AA029134	Human PRO polypept
16	30	76.9	237	22	AA065244	Human PRO511 (UNQ5
17	30	76.9	242	22	AA079067	Human protein seq
18	30	76.9	242	22	AA039926	Human polypeptide
19	30	76.9	254	23	AA079353	Human ovary specif
20	30	76.9	260	21	AA036277	Human protein thalia
21	30	76.9	261	22	AA041712	Human polypeptide
22	30	76.9	262	22	AA073661	Human colon cancer
23	30	76.9	266	22	AA015881	Human novel secret
24	30	76.9	271	21	AA013258	Arabidopsis thalia
25	30	76.9	271	21	AA028883	Arabidopsis thalia
26	30	76.9	290	21	AA036276	Arabidopsis thalia
27	30	76.9	290	21	AA052379	Pseudomonas aerugi
28	30	76.9	296	21	AA028882	Arabidopsis thalia
29	30	76.9	299	21	AA013257	Arabidopsis thalia
30	30	76.9	321	21	AA031332	Arabidopsis thalia
31	30	76.9	337	21	AA009611	Arabidopsis thalia
32	30	76.9	338	21	AA009610	Arabidopsis thalia
33	30	76.9	340	21	AA028881	Arabidopsis thalia
34	30	76.9	342	21	AA031331	Arabidopsis thalia
35	30	76.9	343	21	AA013256	Arabidopsis thalia
36	30	76.9	349	21	AA031330	Arabidopsis thalia
37	30	76.9	381	21	AA009609	Arabidopsis thalia
38	30	76.9	406	23	AA093092	Arabidopsis thalia
39	30	76.9	419	21	AA035460	Arabidopsis thalia
40	30	76.9	452	22	AA092587	Human protein sequ
41	30	76.9	473	21	AA035459	Arabidopsis thalia
42	30	76.9	495	21	AA035458	Arabidopsis thalia
43	30	76.9	582	22	AA061452	Drosophila melanog
44	30	76.9	624	22	AA092857	Human protein sequ
45	30	76.9	646	21	AA031082	Arabidopsis thalia

## ALIGNMENTS

RESULT 1	ABP01599	standard; Protein; 80 AA.
ID	ABP01599	
XX	24-JUN-2002	(first entry)
AC	ABP01599	
XX		
DE	Human ORFX protein sequence SEQ ID NO:3180.	
XX		
XX	Human: open reading frame; ORFX; gene therapy; cancer; cirrhosis;	
KW	hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;	
KW	degenerative disorder; osteoarthritis; neurodegenerative disorder;	
KW	cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;	
KW	hypertension; hypothyroidism; cholesterol ester storage disease;	
KW	immune deficiency; immune disorder; infectious disease;	
KW	autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;	
XX	myasthenia gravis.	
XX		
OS	Homo sapiens.	
XX		
PN	MO200192523-A2.	
XX		
PD	06-DEC-2001.	
XX		
PF	29-MAY-2001; 2001WO-US10836.	
XX		
PR	30-MAY-2000; 2000US-206132P.	
XX		
PR	29-AUG-2000; 2000US-228716P.	
XX		
PA	(CURA-) CURAGEN CORP.	
XX		
XX	Shinkets RA, Leach MD;	
XX		
PI		

XX WPI: 2002-106308/14.  
 DR N-PSDB; ABN17351.  
 XX  
 PT Novel human polypeptides and polynucleotides useful for diagnosing,  
 PT preventing and treating cardiovascular disease, neurodegenerative,  
 PT hyperproliferative disorders and autoimmune disorders -  
 XX  
 PS Disclosure; SEQ ID 3180; 1037p; English.  
 XX  
 CC The present invention describes substantially purified human proteins  
 CC (referred to as open reading frame, ORFX, where x is 1-11491 (see Table 1  
 CC in the specification). ABN15762 to ABN27252 encode the human ORFX  
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for  
 CC treating or preventing a pathology associated with an ORFX-associated  
 CC disorder in humans, and in the manufacture of a medicament for treating a  
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide  
 CC sequences can be used in gene therapy. ORFX sequences can be used in the  
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,  
 CC psoriasis, benign tumors, keloid, degenerative disorders, haemorrhage,  
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ  
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic  
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester  
 CC storage disease, various immune deficiencies and disorders, infectious  
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid  
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host  
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also  
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,  
 CC bone degenerative disorders, or periodontal disease, and for gut  
 CC protection or regeneration and treatment of lung or liver fibrosis,  
 CC reperfusion injury in various tissues and conditions resulting from  
 CC systemic cytokine damage.  
 CC N.B. The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 SQ Sequence 80 AA;  
 QY  
 Db 56 NSSCPCTC 62  
 QY 4 NXSCPXC 10  
 1 1 1 1  
 56 NSSCPCTC 62  
 Query Match 79.5%; Score 31; DB 23; Length 80;  
 Best Local Similarity 57.1%; Pred. No. 2.2e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 RESULT 2  
 AAC03183  
 ID AAG03183 standard; Protein; 84 AA.  
 XX  
 AC AAG03183;  
 XX  
 DT 06-OCT-2000 (first entry)  
 XX  
 DE Human secreted protein, SEQ ID NO: 7264.  
 XX  
 KM Human: 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 KM gene therapy; chromosome mapping.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1033401-A2.  
 XX  
 PD 06-SEP-2000.  
 XX  
 PF 21-FEB-2000; 2000EP-0200610.  
 XX  
 PR 26-FEB-1999; 99US-0122487.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI: 2000-500381/45.  
 DR N-PSDB; AAC03189.  
 XX  
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
 XX  
 PS Claim 13; SEQ ID 7264; 71pp + CD-ROM; English.  
 XX  
 CC The present sequence is a polypeptide encoded by one of a large number  
 CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs  
 CC were prepared from total human RNAs or polyA+ RNAs derived from 30  
 CC different tissues. EST sequences usually correspond mainly to the 3'  
 CC untranslated region (UTR) of the mRNA because they are often obtained  
 CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for  
 CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in  
 CC those cases where longer cDNA sequences have been obtained, the full 5'  
 CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'  
 CC ends and can therefore be used to obtain full length cDNAs and genomic  
 CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and  
 CC chromosome mapping procedures. They are used to obtain upstream  
 CC regulatory sequences and to design expression and secretion vectors.  
 CC  
 SQ Sequence 84 AA;  
 QY  
 Db 20 NSQCPAC 26  
 QY 4 NXSCPXC 10  
 1 1 1 1  
 20 NSQCPAC 26  
 Query Match 76.9%; Score 30; DB 21; Length 84;  
 Best Local Similarity 57.1%; Pred. No. 3.2e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 RESULT 3  
 AAM80051  
 ID AAM80051 standard; Protein; 118 AA.  
 XX  
 AC AAM80051;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human protein SEQ ID NO 3697.  
 XX  
 KM Human: cytokine; cell proliferation; cell differentiation; gene therapy;  
 KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KM tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KM nervous system disorder; arthritis; inflammation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157190-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 05-FEB-2001; 2001WO-US04098.  
 XX  
 PR 03-FEB-2000; 2000US-0496914.  
 PR 27-APR-2000; 2000US-0560875.  
 PR 20-JUN-2000; 2000US-0598075.  
 PR 19-JUL-2000; 2000US-0620325.  
 PR 01-SEP-2000; 2000US-0654936.  
 PR 15-SEP-2000; 2000US-0663561.  
 PR 20-OCT-2000; 2000US-0693325.  
 PR 30-NOV-2000; 2000US-0728422.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y,  
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW,  
 PI Xue AJ, Yang Y, Wejhtman T, Goodrich R;

DR WPI: 2001-476283/51.  
 DR N-PSDB: AAK53184.  
 XX  
 XX Nucleic acids encoding polypeptides with cytokine-like activities,  
 PT useful in diagnosis and gene therapy -  
 PI  
 PI  
 PS Claim 20; Page 414; 6221pp; English.  
 XX  
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the  
 CC encoded polypeptides (AAW78323-AAW80302) that exhibit activity elating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation.  
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666  
 CC (AAW80020) are omitted as the relevant pages from the sequence listing  
 CC were missing at the time of publication.  
 CC  
 XX SQ Sequence 118 AA;  
 Query Match 76.9%; Score 30; DB 22; Length 118;  
 Best Local Similarity 57.1%; Pred. No. 4.1e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 NXXCPXC 10  
 Db 28 NNTCPXC 34  
 RESULT 4 |  
 AAY36293  
 ID AAY36293 standard; Protein: 130 AA.  
 XX  
 AC AAY36293;  
 XX  
 DT 17-SEP-1999 (first entry)  
 XX  
 DE Human secreted protein encoded by gene 70.  
 XX  
 KW Human; secreted protein; cancer; tumour; developmental abnormality;  
 KW autoimmune disease; blood disorder; immune system disorder; inflammation;  
 KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;  
 KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;  
 KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;  
 KW digestive disorder; endocrine disorder; infection; AIDS.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO931117-A1.  
 XX  
 PD 24-JUN-1999.  
 XX  
 PF 17-DEC-1998; 98WO-US27059.  
 XX  
 XX 19-DEC-1997; 97US-0068369.  
 PR 18-DEC-1997; 97US-0068006.  
 PR 18-DEC-1997; 97US-0068007.  
 PR 18-DEC-1997; 97US-0068008.  
 PR 18-DEC-1997; 97US-0068053.  
 PR 18-DEC-1997; 97US-0068054.  
 PR 18-DEC-1997; 97US-0068057.  
 PR 18-DEC-1997; 97US-0068064.  
 PR 18-DEC-1997; 97US-0070923.  
 PR 19-DEC-1997; 97US-0068169.  
 PR 19-DEC-1997; 97US-0068365.  
 PR 19-DEC-1997; 97US-0068367.  
 PR 19-DEC-1997; 97US-0068368.  
 XX

PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Carter KC, Duan RD, Feng P, Ferrie AM, Florence C;  
 PI Florence K, Greene JM, Janat F, Kyaw H, Moore PA;  
 PI Ni J, Rosen CA, Ruben SM, Shi Y, Soppet DR, Wei Y,  
 PI Yu G;  
 XX  
 DR WPI: 1999-418749/35.  
 DR N-PSDB: AAX97985.  
 XX  
 PT New isolated human genes encoding secreted polypeptides  
 XX  
 PS Claim 11; Page 383; 537pp; English.  
 XX  
 CC AAX97916 to AAX98029 represent 110 isolated human secreted protein  
 CC genes. AAY36224 to AAY36727 represent the secreted proteins encoded by  
 CC the 110 human genes. The genes and their corresponding secreted  
 CC polypeptides are useful for preventing, treating or ameliorating medical  
 CC conditions, e.g. by protein or gene therapy. Also pathological conditions  
 CC can be diagnosed by determining the amount of the new polypeptides in a  
 CC sample or by determining the presence of mutations in the new genes.  
 CC Specific uses are described for each of the 110 genes, based on which  
 CC tissues they are most highly expressed in, and include developing  
 CC products for the diagnosis or treatment of cancer, tumours, developmental  
 CC abnormalities and foetal deficiencies, blood disorders, diseases of the  
 CC immune system, autoimmune diseases, inflammation, allergies, Alzheimer's  
 CC and cognitive disorders, schizophrenia, arthritis, asthma, psoriasis,  
 CC sepsis, skin disorders, atherosclerosis, diabetes, cardiovascular  
 CC disorders, kidney disorders, digestive/endocrine disorders, infections  
 CC and AIDS. The polypeptides are also useful for identifying their binding  
 CC partners. The sequences given in AAX97907 to AAX97915 and AAY36223 are  
 CC used in the exemplification of the present invention.  
 CC  
 XX SQ Sequence 130 AA;  
 Query Match 76.9%; Score 30; DB 20; Length 130;  
 Best Local Similarity 57.1%; Pred. No. 4.4e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 NXXCPXC 10  
 Db 32 NSSCPXC 38  
 RESULT 5  
 AAB87620  
 ID AAB87620 standard; protein: 136 AA.  
 XX  
 AC AAB87620;  
 XX  
 DT 15-MAY-2001 (first entry)  
 XX  
 DE Bovine mammary tissue derived protein #11.  
 XX  
 DE Bovine mammary tissue derived protein #11.  
 XX  
 KW Bovine; mammary gland; cancer; tumour; angiogenesis.  
 KW  
 XX Bos taurus.  
 XX  
 OS WO200114553-A1.  
 XX  
 PN 01-MAR-2001.  
 XX  
 PD 23-APR-2000; 2000WO-NZ00166.  
 PF 23-APR-2000; 99US-0150330.  
 XX  
 PR 23-APR-1999; 99US-0150330.  
 XX  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (NZPA-) NEW ZEALAND PASTORAL AGRIC RES INST LTD.  
 XX  
 PI Havukkala IU, Gleen M, Grigor MR, Molenaar AJ;  
 PI WPI: 2001-226619/23.  
 DR  
 XX

PT New polypeptides and polynucleotides encoding the polypeptides, which  
PT are expressed in bovine mammary gland tissue, useful for stimulating  
PT mammary gland growth or function, or inducing differentiation of milk  
PT producing cells  
XX  
XX Claim 11; Page 64; 97pp; English.  
XX  
CC The present invention relates to proteins derived from bovine  
CC mammary gland cells. The invention is useful for stimulating  
CC bovine mammary gland cell growth and function, inhibiting the  
CC growth of various mammary gland cancer cells, inhibiting  
CC angiogenesis and vascularization of tumours, or modulating  
CC the growth of blood vessels in a mammal.  
XX  
XX  
SQ Sequence 136 AA;  
Query Match 76.9%; Score 30; DB 22; Length 136;  
Best Local Similarity 57.1%; Pred. No. 4.5e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 4 NXCPXC 10  
Db 26 NRTCPYC 32  
RESULT 6  
AAU16336  
ID AAU16336 standard; Protein: 147 AA.  
XX  
AC AAU16336;  
XX  
DT 07-NOV-2001 (first entry)  
XX  
DE Human novel secreted protein, Seq ID 1289.  
XX  
XX Human; immunosuppressive; antiarthritic; antihneumatic;  
XX cytoskeletal; cardiact; vasotropic; cerebroprotective; noctropic;  
XX neuroprotective; antibacterial; virucide; fungicide; ophthalmological;  
XX vulnery; secreted protein; rheumatoid arthritis;  
XX hyperproliferative disorder; cardiovascular disorder; cardiac arrest;  
XX cerebrovascular disorder; cerebral ischemia; angiogenesis;  
XX nervous system disorder; Alzheimer's disease; infection; ocular disorder;  
XX corneal infection; wound healing; epithelial cell proliferation;  
XX skin ageing; food additive; preservative; antiproliferative.  
OS Homo sapiens.  
XX  
XX  
XX WO200155322-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01341.  
XX  
XX 31-JAN-2000; 2000US-0179065.  
XX 04-FEB-2000; 2000US-0180628.  
XX 24-FEB-2000; 2000US-0184664.  
XX 02-MAR-2000; 2000US-0186350.  
XX 16-MAR-2000; 2000US-0189874.  
XX 17-MAR-2000; 2000US-0190076.  
XX 18-APR-2000; 2000US-0198123.  
XX 19-MAY-2000; 2000US-0205515.  
XX 07-JUN-2000; 2000US-0209467.  
XX 28-JUN-2000; 2000US-0214886.  
XX 30-JUN-2000; 2000US-0215135.  
XX 07-JUL-2000; 2000US-0216647.  
XX 07-JUL-2000; 2000US-0216880.  
XX 11-JUL-2000; 2000US-0217487.  
XX 11-JUL-2000; 2000US-0217496.  
XX 14-JUL-2000; 2000US-0218290.  
XX 26-JUL-2000; 2000US-0220963.  
XX 26-JUL-2000; 2000US-0220964.  
XX 14-AUG-2000; 2000US-0224518.  
XX 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226868.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235834.  
PR 26-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 27-SEP-2000; 2000US-0235837.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.



PR 27-MAY-1999; 990S-0136392.  
PR 28-MAY-1999; 990S-0136782.  
PR 01-JUN-1999; 990S-0137222.  
PR 03-JUN-1999; 990S-0137528.  
PR 04-JUN-1999; 990S-0137502.  
PR 07-JUN-1999; 990S-0137724.  
PR 08-JUN-1999; 990S-0138094.  
PR 10-JUN-1999; 990S-0138540.  
PR 10-JUN-1999; 990S-0138847.  
PR 14-JUN-1999; 990S-0139119.  
PR 16-JUN-1999; 990S-0139452.  
PR 16-JUN-1999; 990S-0139453.  
PR 17-JUN-1999; 990S-0139492.  
PR 18-JUN-1999; 990S-0139454.  
PR 18-JUN-1999; 990S-0139455.  
PR 18-JUN-1999; 990S-0139456.  
PR 18-JUN-1999; 990S-0139457.  
PR 18-JUN-1999; 990S-0139458.  
PR 18-JUN-1999; 990S-0139459.  
PR 18-JUN-1999; 990S-0139460.  
PR 18-JUN-1999; 990S-0139461.  
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PR 26-JUL-1999; 990S-0145276.  
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PR 03-AUG-1999; 990S-0147038.

PR 04-AUG-1999; 990S-0147204.  
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PR 05-AUG-1999; 990S-0147192.  
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PR 06-AUG-1999; 990S-0147303.  
PR 06-AUG-1999; 990S-0147416.  
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PR 22-SEP-1999; 990S-0155139.  
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PR 21-OCT-1999; 990S-0160814.  
PR 21-OCT-1999; 990S-0160815.  
PR 22-OCT-1999; 990S-0160980.  
PR 22-OCT-1999; 990S-0160981.  
PR 22-OCT-1999; 990S-0160989.  
PR 25-OCT-1999; 990S-0161404.  
PR 25-OCT-1999; 990S-0161405.  
PR 25-OCT-1999; 990S-0161406.  
PR 26-OCT-1999; 990S-0161359.  
PR 26-OCT-1999; 990S-0161360.  
PR 26-OCT-1999; 990S-0161361.  
PR 28-OCT-1999; 990S-0161920.  
PR 28-OCT-1999; 990S-0161992.  
PR 28-OCT-1999; 990S-0161993.







XX Human: immunosuppressive; antiarthritic; antirheumatic;  
KW cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;  
KW neuroprotective; antibacterial; virucide; fungicide; optalmalogical;  
KW vulnerary; secreted protein; rheumatoid arthritis;  
KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;  
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;  
KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;  
KW corneal infection; wound healing; epithelial cell proliferation;  
KW skin ageing; food additive; preservative; antiproliferative.  
XX  
XX Homo sapiens.  
XX  
PN WO200155322-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01341.  
XX  
XX 31-JAN-2000; 2000US-0179065.  
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PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
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 PR 08-DEC-2000; 2000US-0251869.  
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 PR 08-DEC-2000; 2000US-0251989.  
 PR 08-DEC-2000; 2000US-0251990.  
 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0259678.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PT Rosen CA, Barash SC, Ruben SM;  
 PT  
 DR WPI; 2001-488783/53.  
 DR N-PSDB; AAS25870.  
 XX  
 PT New nucleic acid molecules encoding 461 human secreted proteins for  
 PT diagnosing, preventing, treating or ameliorating medical conditions and  
 PT used as food additives or preservatives -  
 XX  
 PS Claim 11: SEQ ID NO 836; 980bp; English.  
 XX  
 CC The invention relates to isolated nucleic acid molecules and their  
 CC encoded secreted proteins. The nucleic acids and proteins are used to  
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They  
 CC are also used in diagnosing a pathological condition or susceptibility  
 CC to a pathological condition. Antibodies to the proteins can also  
 CC be used in alleviating symptoms associated with the disorders and in  
 CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked  
 CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated  
 CC include autoimmune diseases e.g. rheumatoid arthritis,  
 CC hyperproliferative disorders e.g. neoplasms of the breast or liver,  
 CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders  
 CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.  
 CC Alzheimer's disease, infections caused by bacteria, viruses and fungi  
 CC and ocular disorders e.g. corneal infection, and many other  
 CC disorders listed in the specification. The polypeptides can also  
 CC be used to aid wound healing and epithelial cell proliferation, to  
 CC prevent skin aging due to sunburn, to maintain organs before  
 CC transplantation, for supporting cell culture of primary tissues, to  
 CC regenerate tissues and in chemotaxis. The polypeptides can also be used  
 CC as a food additive or preservative to increase or decrease storage  
 CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,  
 CC minerals, cofactors and other nutritional components. The present  
 CC sequence represents a novel secreted protein of the invention.  
 Query Match 76.9%; Score 30; DB 22; Length 201;  
 Best Local Similarity 57.1%; Pred. No. 6e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Oy 4 NXXCPXC 10  
 Db 181 NSTCPIC 187  
 RESULT 11  
 ID AAM25880  
 AC AAM25880; standard; Protein; 231 AA.  
 XX  
 DT 16-OCT-2001 (first entry)  
 XX  
 DE Human protein sequence SEQ ID NO:1395.  
 XX  
 KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;  
 KW antiinflammatory; antirheumatic; antiallergic; immunosuppressive;  
 KW antibacterial; endocrine; cardiant; central nervous system; virucide;  
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antinaemic; anaemia;  
 KW antileggregant; haemostatic; vulnerary; antidiacer; osteopathic; eczema;  
 KW dermatological; antiallergic; antidiabetic; antidiabetic; cyostatic;

KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;  
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;  
 KW antinaphylactic; rheumatoid arthritis; septic shock; pancreatitis;  
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;  
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;  
 KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;  
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;  
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
 KW neurological disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200153455-A2.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 22-DEC-2000; 2000MO-US35017.  
 XX  
 PR 23-DEC-1999; 990S-0471275.  
 PR 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0552317.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PT Tang YT, Liu C, Drmanac RT;  
 PT  
 DR WPI; 2001-457603/49.  
 DR N-PSDB; AAH99821.  
 XX  
 PT Isolated human polynucleotides encoding polypeptides, useful for the  
 PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection -  
 XX  
 PS Claim 20: Page 286; 1217bp; English.  
 XX  
 CC AAH99166 to AAH99904 encode the human proteins given in AAM25225 to  
 CC AAM25963. The proteins can have activities based on the tissues and  
 CC cells they are expressed in, such as: antiinflammatory; antineumatic;  
 CC antiallergic; immunosuppressive; antibacterial; endocrine; cardiant;  
 CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;  
 CC cardiovascular; antinaemic; antileggregant; haemostatic; vulnerary;  
 CC anticancer; osteopathic; dermatological; antiallergic; antidiabetic;  
 CC antidiabetic; cyostatic; neuroprotective; antidepressant; nootropic;  
 CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
 CC encoding them can be used in gene therapy, antisense therapy and vaccine  
 CC production. The proteins and polynucleotides are useful for screening for  
 CC agonists or antagonists of a protein and for the treatment and diagnosis  
 CC of disorders associated with the activity of a protein e.g. inflammation,  
 CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,  
 CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal  
 CC infections, autoimmunity, genetic diseases, haematopoietic disorders,  
 CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,  
 CC osteoporosis, severe combined immunodeficiency, eczema, allergic  
 CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
 CC Alzheimer's disease, Parkinson's disease, neurodegenerative and  
 CC neurological disorders.  
 CC  
 SQ Sequence 231 AA:  
 Query Match 76.9%; Score 30; DB 22; Length 231;  
 Best Local Similarity 57.1%; Pred. No. 6.6e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Oy 4 NXXCPXC 10  
 Db 116 NACCPAC 122  
 RESULT 12  
 ID AAY02654  
 AC AAY02654; standard; Protein; 237 AA.  
 XX  
 AC AAY02654;  
 XX

11-JUN-1999 (first entry)

Human secreted protein encoded by gene 5 clone HCNSP40.

Human; secreted protein; fusion protein; gene therapy; protein therapy; diabetes; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

Homo sapiens.

WO9902546-A1.

21-JAN-1999.

07-JUL-1998; 98WO-US13684.

12-SEP-1997; 97US-0058785.  
PR 08-JUL-1997; 97US-0051916.  
PR 08-JUL-1997; 97US-0051918.  
PR 08-JUL-1997; 97US-0051919.  
PR 08-JUL-1997; 97US-0051920.  
PR 08-JUL-1997; 97US-0051925.  
PR 08-JUL-1997; 97US-0051926.  
PR 08-JUL-1997; 97US-0051928.  
PR 08-JUL-1997; 97US-0051929.  
PR 08-JUL-1997; 97US-0051930.  
PR 08-JUL-1997; 97US-0051931.  
PR 08-JUL-1997; 97US-0052732.  
PR 08-JUL-1997; 97US-0052733.  
PR 08-JUL-1997; 97US-0052793.  
PR 08-JUL-1997; 97US-0052795.  
PR 08-JUL-1997; 97US-0052803.  
PR 18-AUG-1997; 97US-0055684.  
PR 18-AUG-1997; 97US-0055722.  
PR 18-AUG-1997; 97US-0055723.  
PR 18-AUG-1997; 97US-0055947.  
PR 18-AUG-1997; 97US-0055948.  
PR 18-AUG-1997; 97US-0055949.  
PR 18-AUG-1997; 97US-0055950.  
PR 18-AUG-1997; 97US-0055953.  
PR 18-AUG-1997; 97US-0055954.  
PR 18-AUG-1997; 97US-0055964.  
PR 18-AUG-1997; 97US-0055984.  
PR 18-AUG-1997; 97US-0056360.  
PR 12-SEP-1997; 97US-0056660.  
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(HUMA-) HUMAN GENOME SCI INC.

Brewer LA, Ehner R, Fischer CL, Kyaw H, Lafleur DM, Li Y, Moore PA;  
Olson HS, Rosen CA, Ruben SM, Shi Y, Soppet DR, Zeng Z;  
WPI: 1999-120770/10.  
N-PSDB: AAX27315.

New isolated human genes and the secreted polypeptides they encode -  
useful for diagnosis and treatment of e.g. cancers, neurological  
disorders, immune diseases, inflammation or blood disorders

Claim 11: Page 322; 464pp; English.

This sequence represents a secreted human protein encoded by the gene  
clone detailed in the descriptor line. The gene can be used to generate  
fusion proteins by linking to the gene to a human immunoglobulin Fc  
portion (e.g. AAX27302) for increasing the stability of the fused  
protein as compared to the human protein only.

The invention relates to 123 novel genes and their fragments (nucleic  
acid sequences: AAX27311-X27449; amino acid sequences AA02650-Y02788)  
which are useful for preventing, treating or ameliorating medical  
conditions e.g. by protein or gene therapy. Also, pathological  
conditions can be diagnosed by determining the amount of the new  
polypeptides in a sample or by determining the presence of mutations in  
the new polynucleotides. Specific uses are described for each of the 123  
polynucleotides, based on which tissues they are most highly expressed in  
(see AAX27311 for described uses).

Sequence 237 AA;

Query Match 76.9%; Score 30; DB 20; Length 237;  
Best Local Similarity 57.1%; Pred. No. 6.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
DB 122 NAECPAC 128

RESULT 13  
AAX87321  
ID AAX87321 standard; Protein; 237 AA.  
AAX87321;  
11-MAY-2000 (first entry)

Human signal peptide containing protein HSP-98 SEQ ID NO:98.

Human; signal peptide-containing protein; HSP; diagnosis; cancer;  
inflammation; cardiovascular disease; anticancer; anti-inflammatory;  
antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;  
antiallergic; gene therapy; cell proliferation; neurological disorder;  
reproductive disorder; developmental disorder; arteriosclerosis;  
cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;  
asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;  
Parkinson's disease; Huntington's diseases; ovulatory defect;  
muscular dystrophy.

Homo sapiens.

WO200000610-A2.

06-JAN-2000.

25-JUN-1999; 99WO-US14484.

26-JUN-1998; 98US-0090762.  
PR 31-JUL-1998; 98US-0094983.  
PR 01-OCT-1998; 98US-0102886.  
PR 11-DEC-1998; 98US-0112129.

(INCY-) INCYTE PHARM INC.

Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;  
Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;  
Bandman O;  
WPI: 2000-160673/14.  
N-PSDB: AAZ98206.

New human signal peptide-containing proteins useful in treatment,  
prevention and diagnosis of e.g. cancer, inflammation and  
cardiovascular disease

Claim 1: Page 223; 327pp; English.

AA28109 to AA298242 encode AAX87224 to AAX87357 which represent the  
human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have  
anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,  
neuroprotective, cardiovascular and antiallergic activities, and can

CC be used in gene therapy. HSPs can be used to treat or prevent disorders  
CC associated with decreased activity or function of HSP. Antagonists of  
CC HSP are used to treat or prevent disorders associated with increased  
CC activity or function of HSP. Such diseases include cell proliferation  
CC (including cancer), inflammation, cardiovascular, neurological,  
CC reproductive or developmental disorders, (e.g. arteriosclerosis,  
CC cirrhosis, psoriasis), acquired immune deficiency syndrome, anemia,  
CC asthma, Crohn's disease, microbial or other infections, congestive or  
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's  
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP  
CC nucleic acids can be used for the recombinant production of HSP, for  
CC detecting HSP in standard hybridisation and amplification assays (for  
CC diagnosis and monitoring). In gene therapy, as antisense,  
CC triplex-forming or ribozyme therapeutics, for detecting related sequences  
CC or genetic variations, and for chromosomal mapping. HSP are also used to  
CC raise specific antibodies (Ab) and to screen for agonists and  
CC antagonists (potential therapeutic agents). Ab are used to diagnose, or  
CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic  
CC antagonists, in competitive drug screens, and for purification of HSP  
CC from natural sources.

XX Sequence 237 AA;

Query Match 76.9%; Score 30; DB 21; Length 237;  
Best Local Similarity 57.1%; Pred. No. 6.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
| | | |  
Db 122 NAECPAC 128

## RESULT 14

ID AAY66721 standard; protein: 237 AA.

XX AAY66721;

DT 05-APR-2000 (first entry)

XX Membrane-bound protein PRO511.

XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
KW pharmaceutical; receptor immunoadhesin; gene mapping.

XX Homo sapiens.

PN MO9963088-A2.

XX 09-DEC-1999.

XX 02-JUN-1999; 99MO-US12252.

PR 02-JUN-1998; 98US-0087607.

PR 02-JUN-1998; 98US-0087609.

PR 03-JUN-1998; 98US-0087759.

PR 04-JUN-1998; 98US-0088021.

PR 04-JUN-1998; 98US-0088025.

PR 04-JUN-1998; 98US-0088028.

PR 04-JUN-1998; 98US-0088029.

PR 04-JUN-1998; 98US-0088030.

PR 04-JUN-1998; 98US-0088033.

PR 05-JUN-1998; 98US-0088167.

PR 05-JUN-1998; 98US-0088202.

PR 05-JUN-1998; 98US-0088212.

PR 09-JUN-1998; 98US-0088655.

PR 10-JUN-1998; 98US-0088722.

PR 10-JUN-1998; 98US-0088730.

PR 10-JUN-1998; 98US-0088734.

PR 10-JUN-1998; 98US-0088738.

PR 10-JUN-1998; 98US-0088740.

PR 10-JUN-1998; 98US-0088741.

PR 10-JUN-1998; 98US-0088742.

PR 10-JUN-1998; 98US-0088810.

PR 10-JUN-1998; 98US-0088811.

PR 10-JUN-1998; 98US-0088824.

PR 10-JUN-1998; 98US-0088825.

PR 11-JUN-1998; 98US-0088826.

PR 11-JUN-1998; 98US-0088858.

PR 11-JUN-1998; 98US-0088861.

PR 11-JUN-1998; 98US-0088863.

PR 11-JUN-1998; 98US-0088876.

PR 12-JUN-1998; 98US-0089090.

PR 16-JUN-1998; 98US-0089105.

PR 16-JUN-1998; 98US-0089440.

PR 16-JUN-1998; 98US-0089512.

PR 16-JUN-1998; 98US-0089514.

PR 17-JUN-1998; 98US-0089532.

PR 17-JUN-1998; 98US-0089538.

PR 17-JUN-1998; 98US-0089598.

PR 17-JUN-1998; 98US-0089599.

PR 17-JUN-1998; 98US-0089600.

PR 17-JUN-1998; 98US-0089653.

PR 18-JUN-1998; 98US-0089601.

PR 18-JUN-1998; 98US-0089907.

PR 18-JUN-1998; 98US-0089908.

PR 19-JUN-1998; 98US-0089947.

PR 19-JUN-1998; 98US-0089948.

PR 19-JUN-1998; 98US-0089952.

PR 22-JUN-1998; 98US-0090246.

PR 22-JUN-1998; 98US-0090252.

PR 22-JUN-1998; 98US-0090254.

PR 23-JUN-1998; 98US-0090349.

PR 23-JUN-1998; 98US-0090355.

PR 24-JUN-1998; 98US-0090429.

PR 24-JUN-1998; 98US-0090431.

PR 24-JUN-1998; 98US-0090435.

PR 24-JUN-1998; 98US-0090444.

PR 24-JUN-1998; 98US-0090445.

PR 24-JUN-1998; 98US-0090472.

PR 24-JUN-1998; 98US-0090535.

PR 24-JUN-1998; 98US-0090538.

PR 24-JUN-1998; 98US-0090540.

PR 24-JUN-1998; 98US-0090557.

PR 25-JUN-1998; 98US-0090576.

PR 25-JUN-1998; 98US-0090678.

PR 25-JUN-1998; 98US-0090688.

PR 25-JUN-1998; 98US-0090690.

PR 25-JUN-1998; 98US-0090691.

PR 25-JUN-1998; 98US-0090694.

PR 25-JUN-1998; 98US-0090695.

PR 26-JUN-1998; 98US-0090696.

PR 26-JUN-1998; 98US-0090862.

PR 26-JUN-1998; 98US-0090863.

PR 01-JUL-1998; 98US-0091358.

PR 01-JUL-1998; 98US-0091360.

PR 01-JUL-1998; 98US-0091544.

PR 02-JUL-1998; 98US-0091478.

PR 02-JUL-1998; 98US-0091486.

PR 02-JUL-1998; 98US-0091519.

PR 02-JUL-1998; 98US-0091626.

PR 02-JUL-1998; 98US-0091628.

PR 02-JUL-1998; 98US-0091633.

PR 02-JUL-1998; 98US-0091646.

PR 02-JUL-1998; 98US-0091673.

PR 07-JUL-1998; 98US-0091978.

PR 07-JUL-1998; 98US-0091982.

PR 09-JUL-1998; 98US-0092182.

PR 10-JUL-1998; 98US-0092472.

PR 20-JUL-1998; 98US-0093339.

PR 30-JUL-1998; 98US-0094651.

PR 04-AUG-1998; 98US-0095282.

PR 04-AUG-1998; 98US-0095285.  
 PR 04-AUG-1998; 98US-0095301.  
 PR 04-AUG-1998; 98US-0095302.  
 PR 04-AUG-1998; 98US-0095318.  
 PR 04-AUG-1998; 98US-0095321.  
 PR 04-AUG-1998; 98US-0095325.  
 PR 10-AUG-1998; 98US-0095916.  
 PR 10-AUG-1998; 98US-0095929.  
 PR 10-AUG-1998; 98US-0096012.  
 PR 11-AUG-1998; 98US-0096143.  
 PR 11-AUG-1998; 98US-0096146.  
 PR 12-AUG-1998; 98US-0096329.  
 PR 17-AUG-1998; 98US-0096757.  
 PR 17-AUG-1998; 98US-0096766.  
 PR 17-AUG-1998; 98US-0096768.  
 PR 17-AUG-1998; 98US-0096773.  
 PR 17-AUG-1998; 98US-0096791.  
 PR 17-AUG-1998; 98US-0096867.  
 PR 17-AUG-1998; 98US-0096891.  
 PR 17-AUG-1998; 98US-0096894.  
 PR 17-AUG-1998; 98US-0096895.  
 PR 17-AUG-1998; 98US-0096897.  
 PR 18-AUG-1998; 98US-0096949.  
 PR 18-AUG-1998; 98US-0096950.  
 PR 18-AUG-1998; 98US-0096959.  
 PR 18-AUG-1998; 98US-0096960.  
 PR 18-AUG-1998; 98US-0097022.  
 PR 19-AUG-1998; 98US-0097141.  
 PR 20-AUG-1998; 98US-0097218.  
 PR 24-AUG-1998; 98US-0097661.  
 PR 26-AUG-1998; 98US-0097951.  
 PR 26-AUG-1998; 98US-0097952.  
 PR 26-AUG-1998; 98US-0097954.  
 PR 26-AUG-1998; 98US-0097955.  
 PR 26-AUG-1998; 98US-0097971.  
 PR 26-AUG-1998; 98US-0097974.  
 PR 26-AUG-1998; 98US-0097978.  
 PR 26-AUG-1998; 98US-0097979.  
 PR 26-AUG-1998; 98US-0097986.  
 PR 26-AUG-1998; 98US-0098014.  
 PR 31-AUG-1998; 98US-0098325.  
 PR 16-SEP-1998; 98US-0100634.  
 PR 12-JAN-1999; 99US-0115565.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
 PI Wood WI, Yuan J;  
 XX  
 DR WPI: 2000-072883/06.  
 DR N-PSDB; AAZ65061.  
 XX  
 PT Membrane-bound proteins and related nucleotide sequences -  
 PT  
 PS Claim 12; Fig 212; 822pp: English.  
 XX  
 CC The invention provides membrane-bound PRO polypeptides and  
 CC polynucleotides encoding them. The PRO sequences of the invention were  
 CC identified based on extracellular domain homology screening. The PRO  
 CC sequences have homology with proteins including LDL receptors, TIE  
 CC ligands and various enzymes. The membrane-bound proteins and receptor  
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
 CC immunoadhesins, for instance, can be used as therapeutic agents to block  
 CC receptor-ligand interactions. The membrane-bound proteins can also be  
 CC employed for screening of potential peptide or small molecule inhibitors  
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
 CC are useful as hybridization probes, in chromosome and gene mapping and in  
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
 CC will also be useful for the preparation of PRO polypeptides, especially  
 CC by recombinant techniques.  
 CC  
 XX  
 SQ Sequence 237 AA;

Query Match 76.9%; Score 30; DB 21; Length 237;  
 Best Local Similarity 57.1%; Pred. No. 6.7e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 NXXCPXC 10  
 Db 122 NAECFAC 128  
 RESULT 15  
 AAU29134  
 ID AAU29134 standard; Protein; 237 AA.  
 XX  
 AC AAU29134;  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Human PRO polypeptide sequence #111.  
 XX  
 KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200168848-A2.  
 XX  
 PD 20-SEP-2001.  
 XX  
 PF 28-FEB-2001; 2001WO-US06520.  
 XX  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 03-MAR-2000; 2000US-187202P.  
 PR 06-MAR-2000; 2000US-186928P.  
 PR 14-MAR-2000; 2000US-189328P.  
 PR 14-MAR-2000; 2000US-189328P.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 21-MAR-2000; 2000US-190828P.  
 PR 21-MAR-2000; 2000US-191007P.  
 PR 21-MAR-2000; 2000US-191048P.  
 PR 21-MAR-2000; 2000US-191314P.  
 PR 28-MAR-2000; 2000US-192655P.  
 PR 29-MAR-2000; 2000US-193032P.  
 PR 29-MAR-2000; 2000US-193033P.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 04-APR-2000; 2000US-194449P.  
 PR 04-APR-2000; 2000US-194647P.  
 PR 11-APR-2000; 2000US-195975P.  
 PR 11-APR-2000; 2000US-196000P.  
 PR 11-APR-2000; 2000US-196187P.  
 PR 11-APR-2000; 2000US-196690P.  
 PR 11-APR-2000; 2000US-196690P.  
 PR 18-APR-2000; 2000US-198121P.  
 PR 18-APR-2000; 2000US-198585P.  
 PR 25-APR-2000; 2000US-199397P.  
 PR 25-APR-2000; 2000US-199550P.  
 PR 25-APR-2000; 2000US-199654P.  
 PR 03-MAY-2000; 2000US-201516P.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 05-JUN-2000; 2000US-209632P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 22-AUG-2000; 2000US-0644848.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000WO-US34956.  
 XX  
 PA (GETH ) GENENTECH INC.

XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
 PI Pan J, Smith Y, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 XX  
 DR WPI: 2001-602746/68.  
 DR N-PSDB: AAS46035.  
 XX  
 XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 PT presence of tumours, such as prostate and breast tumours, in mammals and  
 PT to screen for modulators of the compounds -  
 XX  
 PS Claim 11; Fig 222; 774pp; English.  
 XX  
 CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
 CC The PRO polypeptides and their associated nucleic acids can be used to  
 CC detect the presence of a tumour in a mammal by comparing the level of  
 CC expression of a PRO polypeptide in a test sample of cells from the animal  
 CC and a control sample of normal cells, whereby a higher level of  
 CC expression in the test sample indicates the presence of a tumour in the  
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
 CC and rabbits but are preferably human. The polypeptides can be used to  
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
 CC when contacted with it. A specific polypeptide can be used to stimulate  
 CC the proliferation or differentiation of chondrocyte cells. The PRO  
 CC proteins can be used to determine the presence of tumours and also  
 CC susceptibility to tumour development, particularly adrenal, lung, colon,  
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders.  
 XX  
 SQ Sequence 237 AA;  
 QY 4 NXXCPC 10  
 DB 122 NAECPC 128

Search completed: December 13, 2002, 08:38:13  
 Job time : 5.63804 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 13, 2002, 08:39:46 ; Search time 14.8221 Seconds  
(without alignments)  
169.748 Million cell updates/sec

Title: US-09-701-080C-18

Perfect score: 851

Sequence: 1 MFODPQERPRKLPOLCTELQ.....WTGRGMSCCRSSRRRETQL 151

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105981 seqs, 16662342 residues

Total number of hits satisfying chosen parameters: 105981

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published\_Applications\_AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEM\_PUB pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PC1\_NEM\_PUB pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEM\_PUB pep:\*  
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13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEM\_PUB pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	843	99.1	273	9	US-10-000-903-4
2	843	99.1	292	9	US-10-000-903-10
3	843	99.1	371	9	US-10-000-903-6
4	843	99.1	390	9	US-10-000-903-14
5	469.5	55.2	278	9	US-10-000-903-21
6	469.5	55.2	383	9	US-10-000-903-23
7	80.5	9.5	256	10	US-09-756-186-2
8	78.5	9.2	552	10	US-09-764-888-183
9	78.5	9.2	553	10	US-09-764-888-163
10	78.5	9.2	4636	10	US-09-835-996A-33
11	77.5	9.1	181	10	US-09-970-532-4
12	77.5	9.1	471	10	US-09-970-532-2
13	77	9.0	285	10	US-09-756-186-6
14	76.5	9.0	162	10	US-09-798-789-18
15	76	8.9	276	10	US-09-764-864-925
16	76	8.9	468	10	US-09-864-761-37991
17	74.5	8.8	153	10	US-09-800-909-3
18	74.5	8.8	153	10	US-09-884-987-4
19	74.5	8.8	153	10	US-09-800-908-12

20	74.5	8.8	161	9	US-09-898-234-4	Sequence 4, Appli
21	74.5	8.8	161	9	US-09-899-429A-4	Sequence 4, Appli
22	74.5	8.8	161	9	US-09-797-356-4	Sequence 4, Appli
23	74.5	8.8	161	10	US-09-889-422-4	Sequence 4, Appli
24	74.5	8.8	161	10	US-09-907-263-2	Sequence 2, Appli
25	74.5	8.8	162	9	US-09-899-429A-6	Sequence 6, Appli
26	74.5	8.8	162	10	US-09-798-789-9	Sequence 2, Appli
27	74.5	8.8	162	10	US-09-798-789-22	Sequence 22, Appli
28	74.5	8.8	172	9	US-09-899-429A-10	Sequence 10, Appli
29	74.5	8.8	173	9	US-09-899-429A-16	Sequence 16, Appli
30	74.5	8.8	183	9	US-09-899-429A-10	Sequence 10, Appli
31	74.5	8.8	190	9	US-09-899-429A-18	Sequence 18, Appli
32	74.5	8.8	200	9	US-09-899-429A-12	Sequence 12, Appli
33	74.5	8.8	201	9	US-09-899-429A-14	Sequence 14, Appli
34	74.5	8.8	211	9	US-09-899-429A-8	Sequence 8, Appli
35	74.5	8.8	336	10	US-09-756-186-8	Sequence 8, Appli
36	74.5	8.8	371	9	US-09-898-234-12	Sequence 12, Appli
37	74.5	8.8	371	10	US-09-792-356-12	Sequence 12, Appli
38	74.5	8.8	371	10	US-09-899-422-12	Sequence 12, Appli
39	74.5	8.8	455	9	US-09-898-234-17	Sequence 17, Appli
40	74.5	8.8	455	9	US-09-756-854-5	Sequence 5, Appli
41	74.5	8.8	455	9	US-09-899-429A-2	Sequence 2, Appli
42	74.5	8.8	455	9	US-09-899-429A-27	Sequence 27, Appli
43	74.5	8.8	455	9	US-10-041-574-5	Sequence 5, Appli
44	74.5	8.8	455	9	US-09-792-356-2	Sequence 2, Appli
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#### ALIGNMENTS

RESULT 1  
US-10-000-903-4  
; Sequence 4, Application US/10000903  
; Publication No. US20020182221A1  
; GENERAL INFORMATION:  
; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabazon Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Fernandez  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Benchelkh, Angela  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45107  
; CURRENT APPLICATION NUMBER: US/10/000,903  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: GB 9717953.5  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 273  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-000-903-4

Query Match 99.1%; Score 843; DB 9; Length 273;  
Best Local Similarity 99.3%; Pred. No. 4.3e-79;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 114 MFODPQERPRKLPOLCTELQTHIHIIIECYVCKQKOLLREYVDFAFRLCIYVBDGNY 173  
QY 61 AVCDKCLKYKSYSEYRHCYSLYGTTEBOQYNNKPLCDLILRCINCKPLCEBCKORHLD 120  
DB 174 AVCDKCLKYKSYSEYRHCYSLYGTTEBOQYNNKPLCDLILRCINCKPLCEBCKORHLD 233  
QY 121 KQRFHINIRGWTGRCMSCRSTRRETQL 151  
DB 234 KQRFHINIRGWTGRCMSCRSTRRETQL 264

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RESULT 2
US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernandez
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Benchel'h, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: prt
; ORGANISM: Homo sapien
US-10-000-903-10

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Query Match	99.1%	Score 843;	DB 9;	Length 282;
Best Local Similarity	99.3%	Pred. No. 4,6e-79;		
Matches 150;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	MFQDPERPRLIPQLCTELQTTIHDIILECYCYCKOOLLREYVDFAFRDLCTIVYRDGNFY	60	
Db	133	MFQDPQERPRKLPQLCTELQTTIHDIILECYCYCKOOLLREYVDFAFRDLCTIVYRDGNFY	192	
QY	61	AVCDKCLFYSKYSYRHHYCSLYCTTLEQOYNKPLCDLLINCINQKRLCPBEKQRHLD	120	
Db	193	AVCDKCLFYSKYSISYRHHYCSLYCTTLEQOYNKPLCDLLINCINQKRLCPBEKQRHLD	252	
QY	121	KKQRFHNIRGAWTGRCMSCCRSSPTRRRETOL	151	
Db	253	KKQRFHNIRGAWTGRCMSCCRSSPTRRRETOL	283	

```

RESULT 3
US-10-000-903-6
; Sequence 6, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Bruck, Claudine
; APPLICANT: Dellisse, Anne-Marie Eva Fernandez
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Benchelkh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRF
; ORGANISM: Homo sapien
; US-10-000-903-6

```

Query Match	99.1%	Score 843	DB 9	Length 371
Best Local Similarly	99.3%	Pred. No. 6e-79		
Matches 150	Conservative 0	Mismatches 1	Indels 0	Gaps 0

0y	1	MEQDQEBPRKLPOLCPELTQTTIHDIILECYCKOOLLREVVQFAFRDLCIVRQSNPY	60
Db	114	MFQDQEBPRKLPOLCPELTQTTIHDIILECYCKOOLLREVVQFAFRDLCIVRQSNPY	173
0y	61	AVCDKCLEKYSKYSBYRHVYCSLVGTTLEQOYNKPLCDLLRINCINCOPLCPBEKORHLD	120
Db	174	AVCDKCLEKYSKYSBYRHVYCSLVGTTLEQOYNKPLCDLLRINCINCOPLCPBEKORHLD	233
0y	121	KQRFHNIRGWTGRCMCCSSRSTRRETOL	151
Db	234	KQRFHNIRGWTGRCMCCSSRSTRRETOL	264

```

RESULT 4
US-10-000-903-14
; Sequence 14, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernando
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Benchelkh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10,000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-14

```

Query Match	99.1%	Score 84.3	DB 9	Length 390
Best Local Similarity	99.3%	Pred. No. 6.4e-79		
Matches 150; Conservative	0	Mismatches 1	Indels 0	Gaps 0
QY	1	MFQDQERPRKLPQCTLEQTITIHDIILECYCKQQLRREYDFAFDLCIYRDGNPY	60	
Db	133	MFQDQERPRKLPQCTLEQTITIHDIILECYCKQQLRREYDFAFDLCIYRDGNPY	192	
QY	61	AVCDKCLAFYSKYSEYRHYCYISLYGTTLEQOYNKPLCDLLIRICINQKPLCPEEKORHLD	120	
Db	193	AVCDKCLAFYSKYSEYRHYCYISLYGTTLEQOYNKPLCDLLIRICINQKPLCPEEKORHLD	252	
QY	121	KKQRFHNIRGRWTGRCMSCCRSSRTTRRQTL	151	
Db	253	KKQRFHNIRGRWTGRCMSCCRSSRTTRRQTL	283	

RESULT 5  
US-10-000-903-21  
; Sequence 21, Application US/10000903  
; Publication NO. US20020182221A1  
; GENERAL INFORMATION:  
; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabezon Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Fernandez  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Bencheikh, Angela  
; TITLE OR INVENTION: Vaccine  
; FILE REFERENCE: B45107  
; CURRENT APPLICATION NUMBER: US/10/000,903  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
; PRIOR FILING DATE: 1998-08-17

PRIOR APPLICATION NUMBER: GB 9717953.5  
 PRIOR FILING DATE: 1997-08-22  
 NUMBER OF SEQ ID NOS: 23  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 21:  
 LENGTH: 278  
 TYPE: PRT  
 ORGANISM: Homo sapien  
 US-10-000-903-21

Query Match: 55.2%; Score 469.5; DB 9; Length 278;  
 Best Local Similarity 56.1%; Pred. No. 6.8e-41;  
 Matches 87; Conservative 22; Mismatches 41; Indels 5; Gaps 1;

QY 2 FDDPDRPKRLPOLCTELTTHIDITLLECYCKQDLREYVDFAFDLCIYRDGNPYA 61  
 DB 115 FEDPTRRPKRLPOLCTELTTHIDITLLECYCKQDLREYVDFAFDLCIYRDGNPYA 174  
 QY 62 VCDKCLKFSKYSEYRHYCYSLVGTTLLEQYNNKPLCDLLIRICINCOKPLCPPEKORHLDK 121  
 DB 175 ACHKCIDFYSRIRELHYSDSYGDTLEKLTNGLYNLILRCLRCOKPLNPAEKLHLMNE 234  
 QY 122 KORFNHIRGRWTRGCMSCCRSSR-----TRRETQL 151  
 DB 235 KRRFNIIAGHYRGCHSCCNRAOERLQRRRETQV 269

# RESULT 6

US-10-000-903-23  
 Sequence 23, Application US/10000903  
 Publication No. US2002018221A1  
 GENERAL INFORMATION:  
 APPLICANT: Bruck, Claudine  
 APPLICANT: Cabazon Silva, Teresa  
 APPLICANT: Delisse, Anne-Marie Eva Fernande  
 APPLICANT: Gerard, Catherine Marie Ghislaine  
 APPLICANT: Lombardo-Bencheikh, Angela  
 TITLE OF INVENTION: Vaccine  
 FILE REFERENCE: B45107  
 CURRENT APPLICATION NUMBER: US/10/000,903  
 CURRENT FILING DATE: 2001-10-01  
 PRIOR APPLICATION NUMBER: PCT/EP98/05285  
 PRIOR FILING DATE: 1998-08-17  
 PRIOR APPLICATION NUMBER: GB 9717953.5  
 PRIOR FILING DATE: 1997-08-22  
 NUMBER OF SEQ ID NOS: 23  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 23  
 LENGTH: 383  
 TYPE: PRT  
 ORGANISM: Homo sapien  
 US-10-000-903-23

Query Match: 55.2%; Score 469.5; DB 9; Length 383;  
 Best Local Similarity 56.1%; Pred. No. 9.7e-41;  
 Matches 87; Conservative 22; Mismatches 41; Indels 5; Gaps 1;

QY 2 FDDPDRPKRLPOLCTELTTHIDITLLECYCKQDLREYVDFAFDLCIYRDGNPYA 61  
 DB 115 FEDPTRRPKRLPOLCTELTTHIDITLLECYCKQDLREYVDFAFDLCIYRDGNPYA 174  
 QY 62 VCDKCLKFSKYSEYRHYCYSLVGTTLLEQYNNKPLCDLLIRICINCOKPLCPPEKORHLDK 121  
 DB 175 ACHKCIDFYSRIRELHYSDSYGDTLEKLTNGLYNLILRCLRCOKPLNPAEKLHLMNE 234  
 QY 122 KORFNHIRGRWTRGCMSCCRSSR-----TRRETQL 151  
 DB 235 KRRFNIIAGHYRGCHSCCNRAOERLQRRRETQV 269

RESULT 7  
 US-09-756-186-2  
 Sequence 2, Application US/09756186

Patent No. US20010014333A1  
 GENERAL INFORMATION:  
 APPLICANT: Campbell, Robert K.  
 APPLICANT: Jameson, Bradford A.  
 APPLICANT: Chappel, Scott C.  
 TITLE OF INVENTION: HYBRID PROTEINS  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BROWDY AND NEIMARK  
 STREET: 419 Seventh Street N.W., Ste. 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 22207  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/756,186  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/804,166  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Browdy, Roger L.  
 REGISTRATION NUMBER: 25,618  
 REFERENCE/DOCKET NUMBER: CAMPBELL-2A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 628-5197  
 TELEFAX: (202) 737-3528  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 256 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-756-186-2

Query Match: 9.5%; Score 80.5; DB 10; Length 256;  
 Best Local Similarity 24.2%; Pred. No. 0.37;  
 Matches 37; Conservative 18; Mismatches 39; Indels 59; Gaps 10;

QY 28 LECYCKQDLREYVDFAFDLCIYRDGNPYAVCDKCLKFSKYSEYRHYCYSLVGT 87  
 DB 82 LSCSKCKREMGVEI-----SSCTVDRD---TVCG-CRK-----NQRHY-----WSEN 121  
 QY 88 LEOQYNNKPLC-----DILIR---CINC--OKPLCPPEKORHLDK 121  
 DB 122 LFQCFNCSLCLNGVHLSQOEKONTVCTCHAGFFLENECVSCGAAPCPECTL---Q 177  
 QY 122 KORFNHIRGRWTRGCMSC-----RSSRT 145  
 DB 178 ENPFSQCAPILQCMGCCFSRAIPTPLRSKT 210

RESULT 8  
 US-09-764-898-183  
 Sequence 183, Application US/09764898  
 Patent No. US2002009673A1  
 GENERAL INFORMATION:  
 APPLICANT: Rosen et al.  
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 FILE REFERENCE: P1201  
 CURRENT APPLICATION NUMBER: US/09/764,898  
 CURRENT FILING DATE: 2001-01-17  
 PRIOR APPLICATION data removed - consult PALM or file wrapper  
 NUMBER OF SEQ ID NOS: 311  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 183

```
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-898-183

Query Match
Best Local Similarity 24.5%; Pred. No. 1.4;
Matches 26; Conservative 11; Mismatches 42; Indels 27; Gaps 6;

OY 51 C1VVRDGNPYAVC-----DKCLKFSKYSEYRHYCYSLYGTTL-----EQOYNK 94
Db 252 C1YTAGNPPCHCOPETGTGRC-----QYVCHHYCVNSSECTTIGDGSVECVCPTRYEG 306

OY 95 PLCDLLIRINCOKPLCPPEEKORHLDKORFHN-IRGRWTGRCMSC 139
Db 307 PKCE-VDKCVCHGCHGHCIIINK-----DSEDIFCNCTNGKIASSCQLC 347

RESULT 9
US-09-764-898-163
; Sequence 163, Application US/09764898
; Patent No. US20020090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P201
; CURRENT APPLICATION NUMBER: US/09/764,898
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 163
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (393)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-898-163

Query Match
Best Local Similarity 24.5%; Pred. No. 1.4;
Matches 26; Conservative 11; Mismatches 42; Indels 27; Gaps 6;

OY 51 C1VVRDGNPYAVC-----DKCLKFSKYSEYRHYCYSLYGTTL-----EQOYNK 94
Db 253 C1YTAGNPPCHCOPETGTGRC-----QYVCHHYCVNSSECTTIGDGSVECVCPTRYEG 307

OY 95 PLCDLLIRINCOKPLCPPEEKORHLDKORFHN-IRGRWTGRCMSC 139
Db 308 PKCE-VDKCVCHGCHGHCIIINK-----DSEDIFCNCTNGKIASSCQLC 348

RESULT 10
US-09-835-996A-33
; Sequence 33, Application US/09835996A
; Patent No. US20020142953A1
; GENERAL INFORMATION:
; APPLICANT: Baillinger, Dennis
; APPLICANT: Loeb, Debra
; APPLICANT: Montgomery, Julie
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Kyle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhao, Qiang
; APPLICANT: Wehman, Tom
; APPLICANT: Drmanac, Radoje
; APPLICANT: Ren, Feiyun
; APPLICANT: Qian, Xiaohong
; APPLICANT: Wang, Dunrui
```

```
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM
; FILE REFERENCE: 28110/35915A
; CURRENT APPLICATION NUMBER: US/09/835,996A
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US 60/197,137
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/714,936
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 09/667,298
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 09/598,042
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 33
; LENGTH: 4636
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-835-996A-33

Query Match
Best Local Similarity 24.5%; Pred. No. 15;
Matches 26; Conservative 11; Mismatches 42; Indels 27; Gaps 6;

OY 51 C1VVRDGNPYAVC-----DKCLKFSKYSEYRHYCYSLYGTTL-----EQOYNK 94
Db 436 C1YTAGNPPCHCOPETGTGRC-----QYVCHHYCVNSSECTTIGDGSVECVCPTRYEG 4390

OY 95 PLCDLLIRINCOKPLCPPEEKORHLDKORFHN-IRGRWTGRCMSC 139
Db 4391 PKCE-VDKCVCHGCHGHCIIINK-----DSEDIFCNCTNGKIASSCQLC 4431

RESULT 11
US-09-970-532-4
; Sequence 4, Application US/09970532
; Patent No. US20020076765A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, J. Michael
; APPLICANT: Kehill, Jr., Marcus
; APPLICANT: Lee, Eun-Kyung
; APPLICANT: Wang, Simon
; TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 08411-018001
; CURRENT APPLICATION NUMBER: US/09/970,532
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 09/513,007
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-970-532-4

Query Match
Best Local Similarity 23.8%; Pred. No. 0.51;
Matches 31; Conservative 20; Mismatches 32; Indels 47; Gaps 10;

OY 28 LECVYCKQQLRREYVFAFRDLC1VVRDGNPYAVCDKCLKFSKYSEYRHYCYSLYGT 87
Db 71 LSCSRCDMEFVEI-----SPCVDRD-----TVCG-CKR-----NOYREY-----WGFT 110

OY 88 LEOOYNKPLCDLLIRINCOKPLCP-----EEOHRHLDKORFHNIRGRWTGRCMSC 139
Db 111 -----GPRCLNCS--LCPNGTVNIPQERDPTTICHGMKFFLKG---ANCISC 153

OY 140 --CRSSRTTR 147
```



OY 148 ETOL 151  
 Db 152 CTXL 155

## RESULT 15

US-09-764-864-925  
 ; Sequence 925, Application US/09764864  
 ; Patent No. US20020132753A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; FILE REFERENCE: PT23  
 ; CURRENT APPLICATION NUMBER: US/09/764,864  
 ; CURRENT FILING DATE: 2001-01-17  
 ; Prior application data removed - consult PALM or file wrapper  
 ; NUMBER OF SEQ ID NOS: 1792  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 925  
 ; LENGTH: 276  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (198)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 ; NAME/KEY: SITE  
 ; LOCATION: (203)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 ; NAME/KEY: SITE  
 ; LOCATION: (229)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 ; NAME/KEY: SITE  
 ; LOCATION: (237)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 ; US-09-764-864-925

## Query Match

8.9%; Score 76; DB 10; Length 276;

Best Local Similarity 25.0%; Pred. No. 1.2;  
 Matches 42; Conservative 16; Mismatches 62; Indels 46; Gaps 11;

OY 3 QDPDERPRKLPQ---LCTELQTTIHDI-----LECVYCKQQLRREYVDFAFRDLCI 52  
 Db 74 KSPGEKPHRCPOCGKCFARKSQLTGHORHSGEHPKCPCEGKRPLRS-----DL-- 124  
 OY 53 VYR-----DGNPYAVCDKCKLAFYSKYSEYRHYCYSLYGTLEBOQYNKPLCDLLRCINC 106  
 Db 125 -YRHQRLHTGERPYE-CTVCKKRFTFRS--HLIGHORTHSEETY-----KCLEP 170  
 OY 107 QKPLC-PEEKORHL-----DKORFHNIRGHWGRCMCCRSSRPTRE 148  
 Db 171 GKSFCHGSSLKRLKLTHTGEEKPHRCN-XGKSFRLTALTLHQRTHTE 217

Search completed: December 13, 2002, 08:46:16  
 Job time : 16.8221 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: December 13, 2002, 08:36:20 ; Search time 48.1718 Seconds  
(without alignments)  
645.878 Million cell updates/sec

Title: US-09-701-080C-18  
Perfect score: 851  
Sequence: 1 MFQDPQERPRKLPQCTELQ.....WTGRCMSCCRSSRRRTQTQL 151

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_21:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriopl:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	843	99.1	151	12	089755 human papil
2	843	99.1	161	12	0919C6 human papil
3	840	98.7	151	12	089852 human papil
4	840	98.7	158	12	09WH13 human papil
5	840	98.7	158	12	08ORD8 human papil
6	840	98.7	158	12	08ORD7 human papil
7	839	98.6	151	12	089640 human papil
8	839	98.6	151	12	09W931 human papil
9	839	98.6	158	12	08QHT0 human papil
10	838	98.5	151	12	09WMP5 human papil
11	838	98.5	158	12	08QHP5 human papil
12	837	98.4	151	12	09W8C3 human papil
13	837	98.4	161	12	0919D4 human papil
14	836	98.2	158	12	09QDH9 human papil
15	836	98.2	158	12	08QRE0 human papil
16	836	98.2	158	12	08QRD9 human papil

17	834	98.0	158	12	09QDH3 human papil
18	834	98.0	158	12	08QRD6 human papil
19	834	98.0	161	12	0919B1 human papil
20	833	97.9	151	12	089648 human papil
21	833	97.9	158	12	08QRE1 human papil
22	832	97.8	151	12	08Q963 human papil
23	831	97.6	151	12	09WMP4 human papil
24	829	97.4	151	12	089887 human papil
25	829	97.4	158	12	09QDH7 human papil
26	829	97.4	158	12	08QRD5 human papil
27	828	97.3	151	12	09WMP2 human papil
28	826	97.1	151	12	012335 human papil
29	826	97.1	151	12	08Q966 human papil
30	824	96.8	151	12	089708 human papil
31	824	96.8	151	12	08QHN0 human papil
32	823	96.7	158	12	09QDH5 human papil
33	822	96.6	161	12	0919A9 human papil
34	818	96.1	151	12	09WMP3 human papil
35	817	96.0	151	12	012336 human papil
36	795	93.4	143	12	0919C4 human papil
37	794	93.3	143	12	0919B6 human papil
38	768	90.2	138	12	0919D2 human papil
39	726	85.3	130	12	0919C2 human papil
40	726	85.3	130	12	0919C0 human papil
41	724	85.1	130	12	0919B4 human papil
42	722	84.8	130	12	0919D0 human papil
43	721	84.7	130	12	0919C8 human papil
44	721	84.7	130	12	0919B8 human papil
45	594	69.8	149	12	084298 human papil

## ALIGNMENTS

RESULT 1

089755 ID 089755 PRELIMINARY: PRT; 151 AA.

AC 089755: 01-NOV-1996 (TREMBLER. 01, Created)

DT 01-NOV-1996 (TREMBLER. 01, Last sequence update)

DT 01-JUN-2001 (TREMBLER. 17, Last annotation update)

DE Early transforming protein E6.

GN E6.

OS Human papillomavirus, and

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI\_TaxID=10566, 10581;

RN [1]

RP SPECIES=Human papillomavirus; STRAIN=OR 6170;

RX MEDLINE=96079021; PubMed=7494284;

RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A., Jensen S.A.;

RT "Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, E7, and L1 coding segments.";

RT J. Virol. 69:7743-7753(1995).

RN [2]

RP SPECIES=Human papillomavirus; STRAIN=OR 6170;

RX Farmer A.D.;

RA Submitted (Aug-1995) to the EMBL/Genbank/DBJ databases.

RN [3]

RP SPECIES=Human papillomavirus type 16; STRAIN=AS, EA7768T, AND EA7496T;

RX van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;

RT "Analysis of Human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotype in cervical carcinogenesis.";

RT Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.

DR EMBL; U34111; AAA91658.1; -.

DR EMBL; U34111; AAA91658.1; -.

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DR EMBL: U34121; AAA91668.1; -
DR EMBL: U34123; AAA91670.1; -
DR EMBL: AJ388056; CAB45124.1; -
DR EMBL: AJ388056; CAB45104.1; -
DR EMBL: AJ388056; CAB45114.1; -
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; F8F62A2FC6BAC02 CRC64;

Query Match 99.1%; Score 843; DB 12; Length 151;
Best Local Similarity 99.3%; Pred. No. 9,4e-85;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MFQDQERRPKLPQCLTETQTTHHIIIECYCKQOLLRREYDFAFRDLCTIVRDGNRY 60
Db 1 MFQDQERRPKLPQCLTETQTTHHIIIECYCKQOLLRREYDFAFRDLCTIVRDGNRY 60

OY 61 AVCDKCLFYSKYSEYRHVCSLYGTTLEEQYKNKPLCDLLIRCIHQKPLCEEKORHID 120
Db 61 AVCDKCLFYSKYSEYRHVCSLYGTTLEEQYKNKPLCDLLIRCIHQKPLCEEKORHID 120

OY 121 KKQRFHNIRGRTWGRCMSSCRSSRTTRETOL 151
Db 121 KKQRFHNIRGRTWGRCMSSCRSSRTTRETOL 151

RESULT 2
O919C6 PRELIMINARY: PRT; 161 AA.
ID ID O919C6 PRELIMINARY: PRT; 161 AA.
AC AC O919C6.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE E6 protein (Fragment).
GN E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
NC NCB1_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16EC6;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RL cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF040697; AAL01351.1; -.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON-TER
SQ SEQUENCE 161 AA; 19628 MW; 15D32F0F12E00460 CRC64;

Query Match 99.1%; Score 843; DB 12; Length 161;
Best Local Similarity 99.3%; Pred. No. 1e-84;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MFQDQERRPKLPQCLTETQTTHHIIIECYCKQOLLRREYDFAFRDLCTIVRDGNRY 60
Db 1 MFQDQERRPKLPQCLTETQTTHHIIIECYCKQOLLRREYDFAFRDLCTIVRDGNRY 70

OY 61 AVCDKCLFYSKYSEYRHVCSLYGTTLEEQYKNKPLCDLLIRCIHQKPLCEEKORHID 120
Db 71 AVCDKCLFYSKYSEYRHVCSLYGTTLEEQYKNKPLCDLLIRCIHQKPLCEEKORHID 130

OY 121 KKQRFHNIRGRTWGRCMSSCRSSRTTRETOL 151
Db 131 KKQRFHNIRGRTWGRCMSSCRSSRTTRETOL 161

RESULT 3
O89852 PRELIMINARY: PRT; 151 AA.
ID ID O89852 PRELIMINARY: PRT; 151 AA.
AC AC O89852.

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QY	121	KKQRFHNIRGWTGRCMCCSSRTRRETQL	151
DT	01-NOV-1996	(TREMBlrel. 01, Created)	
DT	01-NOV-1996	(TREMBlrel. 01, Last sequence update)	
DT	01-JUN-2001	(TREMBlrel. 17, Last annotation update)	
DE	Early transforming protein E6 (Early transforming protein E6 variant).		
DE	Human papillomavirus, and		
OS	Human papillomavirus type 16.		
OS	viruses; dsDNA viruses, no RNA stage; Papillomaviridae; Papillomavirus.		
OC	NCBI_TaxID=10566, 10581;		
ON	[1]		
RP	SEQUENCE FROM N.A.		
RC	SPECIES=Human papillomavirus; STRAIN=OR 8987;		
RX	MEDLINE=96079021; PubMed=7494284;		
RA	Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A., Jenison S.A.;		
RA	"Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, L2, and L1 coding segments.";		
RL	J. Virol. 69:7743-7753(1995).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	SPECIES=Human papillomavirus; STRAIN=OR 8987;		
RA	Farmer A.D.;		
RA	Submitted (Aug-1995) to the EMBL/Genbank/DBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	SPECIES=Human papillomavirus type 16; STRAIN=EC169DEL;		
RA	van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;		
RT	"Analysis of Human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotype in cervical carcinogenesis.";		
RL	Submitted (Jul-1999) to the EMBL/Genbank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RC	SPECIES=Human papillomavirus type 16; STRAIN=VARIOUS STRAINS;		
RA	van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;		
RT	"Analysis of Human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotype in cervical carcinogenesis.";		
RL	Submitted (Jun-1999) to the EMBL/Genbank/DBJ databases.		
RN	[5]		
RP	SEQUENCE FROM N.A.		
RC	SPECIES=Human papillomavirus type 16; STRAIN=XINJIANG;		
RA	Ma Z., Qian D., Ma J., Lin R., Ming W., Zhong Z., Zhang Q., Zhang F.;		
RT	"Cloning and Sequencing of HPV16 E6 gene from Cervical Carcinoma Biopsies in Xinjiang.";		
RL	Shengwu Huaxue Yu Shengwu Wuli Jizhan 0:0-0(2001).		
DR	EMBL, U34134; AAA91681.1; -		
DR	EMBL, U34127; AAA91674.1; -		
DR	EMBL, U34133; AAA91680.1; -		
DR	EMBL, AJ388069; CAB45130.1; -		
DR	EMBL, AJ388057; CAB45106.1; -		
DR	EMBL, AF327851; AAG45940.1; -		
DR	InterPro: IPR001334; E6.		
DR	Pfam: PF00518; E6; 1.		
SO	SEQUENCE 151 AA; 18320 MW; 617D22AFDB4F8C17 CRC64;		
QY	Query Match 98.7%; Score 840; DB 12; Length 151;		
QY	Best Local Similarity 98.7%; Pred. NO. 2e-84;		
QY	Matches 149; Conservative 1; Mismatches 1; Indels 0; Gaps 0;		
QY	1	MEQDQDERPRKLPOLCTELQTTIHDIIEFCVYCKQQLLRREYDFAFRDLCTVYRGNGY	60
DB	1	MEQDQDERPRKLPOLCTELQTTIHDIIEFCVYCKQQLLRREYDFAFRDLCTVYRGNGY	60
QY	61	AVCDGCKLFYSYSEVRHRCYSLVGTTLTBOOYNKPKCDLLINCINOKRPLCEEKORHLD	120
DB	61	AVCDGCKLFYSYSEVRHRCYSLVGTTLTBOOYNKPKCDLLINCINOKRPLCEEKORHLD	120
QY	121	KKQRFHNIRGWTGRCMCCSSRTRRETQL	151



Db 121 KROFNHNRGWTGRCMSCRSSRTRRETOL 151

## RESULT 4

Q9WH13 PRELIMINARY; PRT; 158 AA.  
 AC 09WH13;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DE 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
 DE Isolate 16W12E, complete genome (E6 protein).  
 GN E6.  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10581;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=16W12E;  
 RX MEDLINE=9434235; PubMed=10502513;  
 RA Flores E.R., Allen-Hoffmann B.L., Lee D., Sattler C.A., Lambert P.F.;  
 RT "Establishment of the human papillomavirus type 16 (HPV-16) life cycle  
 in an immortalized human foreskin keratinocyte cell line.";  
 RL Virology 262:344-354(1999).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=16W12E;  
 RA Flores E.R., Nelson J.H., Lambert P.F.;  
 RN Submitted (Feb-1999) to the EMBL/Genbank/DBJ databases.  
 RP (3)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=E-C109G;  
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,  
 RT "Human papillomavirus type 16 intratypic variant infection and risk  
 for cervical neoplasia in Southern China.";  
 RL Submitted (Feb-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF125673; AAD33252.1; -  
 DR EMBL: AF486322; AAL96623.1; -  
 DR InterPro: IPR001334; E6.  
 DR Pfam: PF00518; E6; 1.  
 SO SEQUENCE 158 AA; 19173 MW; 9F0CF5ADDA2ED7FE CRC64;

Query Match 98.7%; Score 840; DB 12; Length 158;  
 Best local Similarity 98.7%; Pred. No. 2.1e-84;  
 Matches 149; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIILCEVCYCKQOLLREYVDFAFRDLCIYRGDGNPY 60  
 Db 8 MFODPQERPRKLPOLCTELQTTIHDIILCEVCYCKQOLLREYVDFAFRDLCIYRGDGNPY 67  
 QY 61 AVCDKCLKFSKYSERHYCYSLYGTLLLEQYKPKLDCDLIRINCOKPLCPPEKORHLD 120  
 Db 68 AVCDKCLKFSKYSERHYCYSLYGTLLLEQYKPKLDCDLIRINCOKPLCPPEKORHLD 127  
 QY 121 KROFNHNRGWTGRCMSCRSSRTRRETOL 151  
 Db 128 KROFNHNRGWTGRCMSCRSSRTRRETOL 158

RESULT 5  
 Q8ORD8 PRELIMINARY; PRT; 158 AA.  
 AC 08ORD8;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, last sequence update)  
 DE 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
 DE E6 protein.  
 GN E6.  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10581;

RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=E-G449T;  
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,  
 RT "Human papillomavirus type 16 intratypic variant infection and risk  
 for cervical neoplasia in Southern China.";  
 RL Submitted (Feb-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF486316; AAL96623.1; -  
 SO SEQUENCE 158 AA; 19188 MW; 01FEF51D21A7EB CRC64;

Query Match 98.7%; Score 840; DB 12; Length 158;  
 Best local Similarity 98.7%; Pred. No. 2.1e-84;  
 Matches 149; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIILCEVCYCKQOLLREYVDFAFRDLCIYRGDGNPY 60  
 Db 8 MFODPQERPRKLPOLCTELQTTIHDIILCEVCYCKQOLLREYVDFAFRDLCIYRGDGNPY 67  
 QY 61 AVCDKCLKFSKYSERHYCYSLYGTLLLEQYKPKLDCDLIRINCOKPLCPPEKORHLD 120  
 Db 68 AVCDKCLKFSKYSERHYCYSLYGTLLLEQYKPKLDCDLIRINCOKPLCPPEKORHLD 127  
 QY 121 KROFNHNRGWTGRCMSCRSSRTRRETOL 151  
 Db 128 KROFNHNRGWTGRCMSCRSSRTRRETOL 158

## RESULT 6

Q8ORD7 PRELIMINARY; PRT; 158 AA.  
 AC 08ORD7;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, last sequence update)  
 DE 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
 DE E6 protein.  
 GN E6.  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10581;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=E-C442T;  
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,  
 RT "Human papillomavirus type 16 intratypic variant infection and risk  
 for cervical neoplasia in Southern China.";  
 RL Submitted (Feb-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF486318; AAL96623.1; -  
 SO SEQUENCE 158 AA; 19173 MW; 14EBF5ADCFDB3640 CRC64;

Query Match 98.7%; Score 840; DB 12; Length 158;  
 Best local Similarity 98.7%; Pred. No. 2.1e-84;  
 Matches 149; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIILCEVCYCKQOLLREYVDFAFRDLCIYRGDGNPY 60  
 Db 8 MFODPQERPRKLPOLCTELQTTIHDIILCEVCYCKQOLLREYVDFAFRDLCIYRGDGNPY 67  
 QY 61 AVCDKCLKFSKYSERHYCYSLYGTLLLEQYKPKLDCDLIRINCOKPLCPPEKORHLD 120  
 Db 68 AVCDKCLKFSKYSERHYCYSLYGTLLLEQYKPKLDCDLIRINCOKPLCPPEKORHLD 127  
 QY 121 KROFNHNRGWTGRCMSCRSSRTRRETOL 151  
 Db 128 KROFNHNRGWTGRCMSCRSSRTRRETOL 158

## RESULT 7

Q89640 PRELIMINARY; PRT; 151 AA.  
 AC 089640;  
 OX 089640;

DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 RT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE Early transforming protein E6.  
 GN E6.  
 OS Human papillomavirus.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10566;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-OR 7574;  
 RX MEDLINE=96079021; Pubmed=7494284;  
 RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,  
 Jensen S.A.;  
 RT "Human papillomavirus type 16 variant lineages in United States  
 RT populations characterized by nucleotide sequence analysis of the E6,  
 RT L2, and L1 coding segments";  
 RL J. Virol. 69:7743-7753(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-OR 7574;  
 RA Farmer A.D.;  
 RU Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U34129; AAA91676.1; -;  
 DR EMBL; U34115; AAA91662.1; -;  
 DR EMBL; U34120; AAA91667.1; -;  
 DR EMBL; U34124; AAA91671.1; -;  
 DR InterPro: IPR001334; E6.  
 DR Pfam: PF00518; E6; 1.  
 SQ SEQUENCE 151 AA; 18348 MW; FE3F2A2FCF0A6CB2 CRC64;

Query Match 98.6%; Score 839; DB 12; Length 151;  
 Best Local Similarity 98.7%; Pred. No. 2.6e-84;  
 Matches 149; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQOQLLRREYDFARFDCIYRDGNPY 60  
 DB 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQOQLLRREYDFARFDCIYRDGNPY 60  
 QY 61 AVCCKCLFYSKSEYRHYCYSLGTTLEOYKNPCLDCLIRINCOKPLCPPEKORHLD 120  
 DB 61 AVCCKCLFYSKSEYRHYCYSLGTTLEOYKNPCLDCLIRINCOKPLCPPEKORHLD 120  
 QY 121 KKORFHNIRGRWGTGRMCCSCSSRTRETOL 151  
 DB 121 KKORFHNIRGRWGTGRMCCSCSSRTRETOL 151

RESULT 8  
 Q9W931  
 ID Q9W931 PRELIMINARY; PRT; 151 AA.  
 AC Q9W931;  
 DT 01-NOV-1999 (TReMBLrel. 12, Created)  
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
 RT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE E6 protein.  
 GN E6.  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10581;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-EA246T 2;  
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,  
 Verheljen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
 RT "Analysis of Human papillomavirus type 16 E6 variants in relation to  
 RT p53 codon 72 polymorphism genotype in cervical carcinogenesis";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ388059; CAB45110.1; -;  
 DR EMBL; AJ388058; CAB45108.1; -;  
 DR InterPro: IPR001334; E6.

DR Pfam: PF00518; E6; 1.  
 SQ SEQUENCE 151 AA; 18306 MW; 6FB3D9E0F24A5300 CRC64;  
 Query Match 98.6%; Score 839; DB 12; Length 151;  
 Best Local Similarity 98.7%; Pred. No. 2.6e-84;  
 Matches 149; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQOQLLRREYDFARFDCIYRDGNPY 60  
 DB 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQOQLLRREYDFARFDCIYRDGNPY 60  
 QY 61 AVCCKCLFYSKSEYRHYCYSLGTTLEOYKNPCLDCLIRINCOKPLCPPEKORHLD 120  
 DB 61 AVCCKCLFYSKSEYRHYCYSLGTTLEOYKNPCLDCLIRINCOKPLCPPEKORHLD 120  
 QY 121 KKORFHNIRGRWGTGRMCCSCSSRTRETOL 151  
 DB 121 KKORFHNIRGRWGTGRMCCSCSSRTRETOL 151

RESULT 9  
 Q9W931  
 ID Q9W931 PRELIMINARY; PRT; 158 AA.  
 AC Q9W931;  
 DT 01-JUN-2002 (TReMBLrel. 21, Created)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
 RT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE E6 protein.  
 GN E6.  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10581;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-AS-P, AS-C193, AND AS-A178;  
 RA Chan P.K.-S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,  
 Cheung J.L.K., Xu L.Y., Cheng A.F.;  
 RT "Human papillomavirus type 16 intra-typic variant infection and risk  
 RT for cervical neoplasia in Southern China";  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF486399; AAL96604.1; -;  
 DR EMBL; AF486300; AAL96605.1; -;  
 DR EMBL; AF486301; AAL96606.1; -;  
 DR EMBL; AF486302; AAL96607.1; -;  
 DR EMBL; AF486306; AAL96611.1; -;  
 DR EMBL; AF486308; AAL96613.1; -;  
 SQ SEQUENCE 158 AA; 19201 MW; 004EF5ADC6B375B CRC64;

Query Match 98.6%; Score 839; DB 12; Length 158;  
 Best Local Similarity 98.7%; Pred. No. 2.7e-84;  
 Matches 149; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQOQLLRREYDFARFDCIYRDGNPY 60  
 DB 8 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQOQLLRREYDFARFDCIYRDGNPY 67  
 QY 61 AVCCKCLFYSKSEYRHYCYSLGTTLEOYKNPCLDCLIRINCOKPLCPPEKORHLD 120  
 DB 68 AVCCKCLFYSKSEYRHYCYSLGTTLEOYKNPCLDCLIRINCOKPLCPPEKORHLD 127  
 QY 121 KKORFHNIRGRWGTGRMCCSCSSRTRETOL 151  
 DB 128 KKORFHNIRGRWGTGRMCCSCSSRTRETOL 158

RESULT 10  
 Q9W931  
 ID Q9W931 PRELIMINARY; PRT; 151 AA.  
 AC Q9W931;  
 DT 01-NOV-1999 (TReMBLrel. 12, Created)  
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
 RT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)



FT NON\_TER 1 1  
SQ SEQUENCE 161 AA; 19624 MW; 10C72CDB14200460 CRC64;

Query Match  
Best Local Similarity 98.4%; Score 837; DB 12; Length 161;

Matches 148; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOQLLRREYDFAFRDLCTIYRDGNPY 60  
DB 11 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOQLLRREYDFAFRDLCTIYRDGNPY 70  
QY 61 AVCDKCLKFYSKISEYRHYCYSLVGTLEQYKNPLCDLLIRINCINCKPLCPPEKQKHLD 120  
DB 71 AVCDKCLKFYSKISEYRHYCYSLVGTLEQYKNPLCDLLIRINCINCKPLCPPEKQKHLD 130  
QY 121 KKORFHNIRGHWIGRCMSCCRSSRTRETOL 151  
DB 131 KKORFHNIRGHWIGRCMSCCRSSRTRETOL 161

## RESULT 14

Q9QDH9 PRELIMINARY; PRT; 158 AA.

AC Q9QDH9;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE E6 protein.  
GN E6.  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10581;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=KE6-1;  
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;  
RT "The most commonly found Human Papillomavirus type 16 E6 and E7  
sequence variation tend to occur together."  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AS-C442;  
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan K.Y.M.,  
RT "Human papillomavirus type 16 intra-typic variant infection and risk  
for cervical neoplasia in Southern China."  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF187866; AAF13392.1; -;  
DR EMBL; AF486304; AAL96609.1; -;  
DR EMBL; AF486305; AAL96610.1; -;  
DR InterPro: IPR001334; E6.  
DR Pfam: PF00518; E6; 1.  
SQ SEQUENCE 158 AA; 19187 MW; 155BF5ADCE6B36F0 CRC64;

Query Match  
Best Local Similarity 98.2%; Score 836; DB 12; Length 158;

Matches 148; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOQLLRREYDFAFRDLCTIYRDGNPY 60  
DB 8 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOQLLRREYDFAFRDLCTIYRDGNPY 67  
QY 61 AVCDKCLKFYSKISEYRHYCYSLVGTLEQYKNPLCDLLIRINCINCKPLCPPEKQKHLD 120  
DB 68 AVCDKCLKFYSKISEYRHYCYSLVGTLEQYKNPLCDLLIRINCINCKPLCPPEKQKHLD 127  
QY 121 KKORFHNIRGHWIGRCMSCCRSSRTRETOL 151  
DB 128 KKORFHNIRGHWIGRCMSCCRSSRTRETOL 158

RESULT 15,

Q8QREO  
ID Q8QREO PRELIMINARY; PRT; 158 AA.

AC Q8QREO;  
DT 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE E6 protein.

GN E6.

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI\_TaxID=10581;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=AS-G137;

RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,

RT "Human papillomavirus type 16 intra-typic variant infection and risk

for cervical neoplasia in Southern China."

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF486307; AAL96612.1; -;

SQ SEQUENCE 158 AA; 19187 MW; 005E2FC1E617C55B CRC64;

Query Match  
Best Local Similarity 98.2%; Score 836; DB 12; Length 158;

Matches 148; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOQLLRREYDFAFRDLCTIYRDGNPY 60  
DB 8 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOQLLRREYDFAFRDLCTIYRDGNPY 67  
QY 61 AVCDKCLKFYSKISEYRHYCYSLVGTLEQYKNPLCDLLIRINCINCKPLCPPEKQKHLD 120  
DB 68 AVCDKCLKFYSKISEYRHYCYSLVGTLEQYKNPLCDLLIRINCINCKPLCPPEKQKHLD 127  
QY 121 KKORFHNIRGHWIGRCMSCCRSSRTRETOL 151  
DB 128 KKORFHNIRGHWIGRCMSCCRSSRTRETOL 158

Search completed: December 13, 2002, 08:39:39  
Job time : 50.1718 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 13, 2002, 08:31:40 ; Search time 15.7485 Seconds  
(Without alignments)  
397.685 Million cell updates/sec

Title: US-09-701-080c-18

Sequence: 1 MFQDDPQERPRKILPOLCTELQ.....WTGRCMSCCRSRTRETQL 151

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	843	99.1	158	1	VE6_HPVI6
2	592	69.6	149	1	VE6_HPVI3
3	538	63.2	149	1	VE6_HPVI3
4	534	62.7	149	1	VE6_HPVI3
5	516	60.6	149	1	VE6_HPVI3
6	507	59.6	148	1	VE6_HPVI3
7	499	58.6	148	1	VE6_HPVI3
8	483.5	56.8	158	1	VE6_HPVI3
9	482.5	56.7	158	1	VE6_HPVI3
10	474	55.7	151	1	VE6_HPVI3
11	473.5	55.6	158	1	VE6_HPVI3
12	469.5	55.2	158	1	VE6_HPVI3
13	465.5	54.7	158	1	VE6_HPVI3
14	463.5	54.5	158	1	VE6_HPVI3
15	454	53.3	191	1	VE6_HPVI3
16	450.5	52.9	150	1	VE6_HPVI3
17	441.5	51.9	155	1	VE6_HPVI3
18	406.5	47.8	153	1	VE6_HPVI3
19	394	46.3	154	1	VE6_HPVI3
20	387.5	45.5	155	1	VE6_HPVI3
21	342.5	40.2	155	1	VE6_HPVI3
22	322	37.8	153	1	VE6_HPVI3
23	321	37.7	150	1	VE6_HPVI3
24	320	37.6	150	1	VE6_HPVI3
25	318	37.4	150	1	VE6_HPVI3
26	316.5	37.2	153	1	VE6_HPVI3
27	315	37.0	144	1	VE6_HPVI3
28	311	36.5	159	1	VE6_HPVI3
29	310	36.4	150	1	VE6_HPVI3
30	307.5	36.1	154	1	VE6_HPVI3
31	305.5	35.9	154	1	VE6_HPVI3
32	305	35.8	150	1	VE6_HPVI3
33	300	35.3	142	1	VE6_HPVI3

34	289	34.0	150	1	VE6_HPVI3	002269 human papill
35	284	33.4	150	1	VE6_HPVI3	P27228 human papill
36	281	33.0	146	1	VE6_HPVI3	P08094 human papill
37	260	30.6	146	1	VE6_HPVI3	P50802 human papill
38	257	30.2	148	1	VE6_HPVI3	P36802 human papill
39	257	30.2	148	1	VE6_HPVI3	P50803 human papill
40	252	29.6	152	1	VE6_HPVI3	P36729 human papill
41	196.5	23.1	165	1	VE6_HPVI3	P50775 human papill
42	196	23.0	140	1	VE6_HPVI3	P00785 human papill
43	192	22.6	140	1	VE6_HPVI3	P50777 human papill
44	189.5	22.3	157	1	VE6_HPVI3	P50776 human papill
45	188.5	22.2	142	1	VE6_HPVI3	P08092 human papill

## ALIGNMENTS

RESULT 1	ID	VE6_HPVI6	STANDARD:	PRT:	158 AA.
AC	P03126:				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	E6 protein.				
GN	E6				
OS	Human papillomavirus type 16.				
OC	Viruses; dsDNA viruses, no RNA stage: Papillomaviridae;				
OC	Papillomavirus.				
OX	NCBI_TaxID=10581;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=85246220; PubMed=2990099;				
RA	Seedorf K., Krammer G., Durst W., Suhai S., Roweckamp W.G.;				
RT	"Human papillomavirus type 16 DNA sequence.";				
RL	Virology 145:181-185(1985).				
RN	[2]				
RP	SEQUENCE OF 150 FROM N.A.				
RX	MEDLINE=90218027; PubMed=2157796;				
RA	Schneider-Maunoury S., Penau-Arnaudet G., Breitburd F., Orth G.;				
RT	"Expression of the human papillomavirus type 16 genome in SK-V cells,				
RL	a line derived from a vulvar intraepithelial neoplasia.";				
CC	J. Gen. Virol. 71:809-817(1990).				
CC	-1- FUNCTION: THIS PROTEIN HAS TRANSFORMING ACTIVITY IN VITRO.				
CC	-1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE				
CC	STRANDED DNA (IN VITRO).				
CC	-1- SUBCELLULAR LOCATION: Nuclear matrix-associated.				
CC	-1- SUBCELLULAR LOCATION: HPV16, IN COMPARISON TO HPV TYPES 6 AND 11, IS MORE				
CC	OFTEN ASSOCIATED WITH MALIGNANT GENITAL CANCERS IN HUMANS.				
CC	-----				
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	use by non-profit institutions as long as its content is in no way				
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
CC	-----				
DR	EMBL; K02718; AAA46939.1; -				
DR	EMBL; D00735; BAA00632.1; -				
DR	PIR; A03682; W6MLHS.				
DR	InterPro: IPR001334; E6.				
DR	Pfam; PF00518; E6; 1.				
KW	Early protein; DNA-binding; Nuclear protein; Zinc-finger;				
KW	Oncogene.				
FT	ZN-FING 37 73				POTENTIAL.
FT	ZN-FING 110 146				POTENTIAL.
FT	SEQUENCE 158 AA; 19187 MW; 01FE5A0CFDB37EB CRC64;				
SO	Query Match				99.1%; Score 843; DB 1; Length 158;
	Best Local Similarity				99.3%; Pred. No. 5.2e-74;
	Matches 150; Conservative				0; Mismatches 1; Indels 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIILCEVCYCKOOLLREYVDFAFRDLCTIVYRDGNPY 60  
 DB 8 MFODPOERPRKLPOLCTELQTTIHDIILCEVCYCKOOLLREYVDFAFRDLCTIVYRDGNPY 67  
 QY 61 AVCDKCLAFYSKSEYRHYCYSLYGTTLFQOYKPKPLCDLLIRINCQKPLCPPEKQRHLD 120  
 DB 68 AVCDKCLAFYSKSEYRHYCYSLYGTTLFQOYKPKPLCDLLIRINCQKPLCPPEKQRHLD 127  
 QY 121 KKRFHNIIGRWTRGCMSCCRSSRTRETOL 151  
 DB 128 KKRFHNIIGRWTRGCMSCCRSSRTRETOL 158

RESULT 2  
 VEG\_HPV35  
 ID VEG\_HPV35 STANDARD: PRT: 149 AA.  
 AC P27228:

DT 01-AUG-1992 (rel. 23, Created)  
 DT 01-AUG-1992 (rel. 23, Last sequence update)  
 DT 15-JUN-2002 (rel. 41, Last annotation update)  
 DE E6 protein.

OS Human papillomavirus type 35.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.

OX NCBI\_TaxID=10587;

RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=94265501; PubMed=8205838;

RA Dellus H., Hofmann B.;  
 RT Primer-directed sequencing of human papillomavirus types.;

RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).

RN [2]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=92124753; PubMed=1310198;

RA Marich J.E., Pontsler A.V., Rice S.M., McGraw K.A., Dubensky T.W.;

RT The phylogenetic relationship and complete nucleotide sequence of

human papillomavirus type 35.;

VL Virology 186:770-776(1992).

CC -1- FUNCTION: THIS PROTEIN MAY BE INVOLVED IN THE ONCOGENIC POTENTIAL

OF THIS VIRUS (ASSOCIATED WITH CANCER OF THE UTERINE CERVIX).

CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE

STRANDED DNA (IN VITRO).

CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.

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DR EMBL: X74477; CA52561.1; -

DR EMBL: M74117; AAA46966.1; -

DR PIR: E40824; W6WJ35.

DR PIR: S36521; S36521.

DR InterPro: IPR001334; E6.

DR Pfam: PF00518; E6; 1.

KW Early protein; DNA-binding; Nuclear protein; Zinc-finger;

KW Oncogene.

FT ZN\_FING 30 66

FT ZN\_FING 103 139

FT ZN\_FING 149 180

FT ZN\_FING 180 45

FT ZN\_FING 45 66

FT ZN\_FING 66 139

FT ZN\_FING 139 180

FT ZN\_FING 180 45

FT ZN\_FING 45 66

FT ZN\_FING 66 139

FT ZN\_FING 139 180

FT ZN\_FING 180 45

QY 61 AVCDKCLAFYSKSEYRHYCYSLYGTTLFQOYKPKPLCDLLIRINCQKPLCPPEKQRHLD 120  
 DB 61 GVCMKCLAFYSKSEYRHYCYSLYGTTLFQOYKPKPLCDLLIRINCQKPLCPPEKQRHLD 120  
 QY 121 KKRFHNIIGRWTRGCMSCCRSSRTRETOL 151  
 DB 121 KKRFHNIIGRWTRGCMSCCRSSRTRETOL 151

RESULT 3  
 VEG\_HPV31  
 ID VEG\_HPV31 STANDARD: PRT: 149 AA.  
 AC P17386;

DT 01-AUG-1990 (rel. 15, Created)  
 DT 01-AUG-1990 (rel. 15, Last sequence update)  
 DT 15-JUN-2002 (rel. 41, Last annotation update)  
 DE E6 protein.

OS Human papillomavirus type 31.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.

OX NCBI\_TaxID=10585;

RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=89299478; PubMed=2545036;

RA Goldsborough M.D., Disilvestre D., Temple G.F., Lorincz A.T.;

RT Nucleotide sequence of human papillomavirus type 31: a cervical

neoplasia-associated virus.;

VL Virology 171:306-311(1989).

CC -1- FUNCTION: THIS PROTEIN MAY BE INVOLVED IN THE ONCOGENIC POTENTIAL

OF THIS VIRUS (CERVICAL NEOPLASIA-ASSOCIATED VIRUS).

CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE

STRANDED DNA (IN VITRO).

CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.

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DR EMBL: J04353; AAA46950.1; -

DR PIR: A32444; W6WJ31.

DR InterPro: IPR001334; E6.

DR Pfam: PF00518; E6; 1.

KW Early protein; DNA-binding; Nuclear protein; Zinc-finger;

KW Oncogene.

FT ZN\_FING 30 66

FT ZN\_FING 103 139

FT ZN\_FING 149 180

FT ZN\_FING 180 45

FT ZN\_FING 45 66

FT ZN\_FING 66 139

FT ZN\_FING 139 180

FT ZN\_FING 180 45

FT ZN\_FING 45 66

FT ZN\_FING 66 139

FT ZN\_FING 139 180

FT ZN\_FING 180 45

FT ZN\_FING 45 66

FT ZN\_FING 66 139

FT ZN\_FING 139 180

FT ZN\_FING 180 45

FT ZN\_FING 45 66

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AC P06427;
DR 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE E6 protein.
GN E6.
OS Human papillomavirus type 33.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10586;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86200464; PubMed=3009902;
RA Cole S.T., Strecek R.E.;
RT "Genome organization and nucleotide sequence of human papillomavirus
RT type 33, which is associated with cervical cancer.";
RL J. Virol. 58:991-995(1986).
CC -1- FUNCTION: THIS PROTEIN MAY BE INVOLVED IN THE ONCOGENIC POTENTIAL
CC OF THIS VIRUS (CERVICAL NEOPLASIA-ASSOCIATED VIRUS).
CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC STRANDED DNA (IN VITRO).
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.
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CC
CC -----
CC DR EMBL, M12732; AAA46958.1; -.
CC DR PIR, A03683; W6WL33.
CC DR InterPro: IPR001334; E6.
CC DR Pfam: PF00518; E6; 1.
CC DR Early protein; DNA-binding; Nuclear protein; Zinc-finger;
CC Oncogene.
CC KW ZN_FING 30 66 POTENTIAL.
CC FT ZN_FING 103 139 POTENTIAL.
CC SQ SEQUENCE 149 AA; 17652 MW; EDDB7444F9C8B1AF CRC64;

Query Match
Best Local Similarity 62.7%; Score 534; DB 1; Length 149;
Matches 96; Conservative 20; Mismatches 33; Indels 2; Gaps 1;

OY 1 MFOQDERRRKLPOLCTELQTHIHDIIECYCKQOQLRREYDFAFRLDCTVYRDGNPY 60
DB 1 MFOQDERRRKLPOLCTELQTHIHDIIECYCKQOQLRREYDFAFRLDCTVYRDGNPY 60
OY 61 AVCDKCLAFKYSKYSERHRCYSLYGTTLEQYNNKPLCDLLIRINCQKPLCEKORHND 120
DB 61 AVCDKCLAFKYSKYSERHRCYSLYGTTLEQYNNKPLCDLLIRINCQKPLCEKORHND 120
OY 61 GICKLCLRLSKISEYRHNYSLYGTLEQYNNKPLCDLLIRINCQKPLCEKORHND 120
DB 61 GICKLCLRLSKISEYRHNYSLYGTLEQYNNKPLCDLLIRINCQKPLCEKORHND 120
OY 121 KKQRFNINGRWGTGRCMSCCRSSRTRETQL 151
DB 121 KKQRFNINGRWGTGRCMSCCRSSRTRETQL 151
OY 121 LNKRFNINSGRWGRCACWRR--RRRTQL 149
DB 121 LNKRFNINSGRWGRCACWRR--RRRTQL 149

RESULT 5
VE6_HPV58 STANDARD; PRT; 149 AA.
AC P26555;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE E6 protein.
GN E6.
OS Human papillomavirus type 58.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10598;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=92024102; PubMed=1656594;
RA Kiri T., Iwamoto S., Matsukura T.;
RT "Human papillomavirus type 58 DNA sequence.";
RL Virology 185:424-427(1991).
CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC STRANDED DNA (IN VITRO).
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC
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CC
CC -----
CC DR EMBL, D90400; BAA1845.1; -.
CC DR PIR, E36779; W6WL58.
CC DR InterPro: IPR001334; E6.
CC DR Pfam: PF00518; E6; 1.
CC DR Early protein; DNA-binding; Nuclear protein; Zinc-finger.
CC KW ZN_FING 30 66 POTENTIAL.
CC FT ZN_FING 103 139 POTENTIAL.
CC SQ SEQUENCE 149 AA; 17794 MW; 79B3DC9583B158 CRC64;

Query Match
Best Local Similarity 60.6%; Score 516; DB 1; Length 149;
Matches 95; Conservative 19; Mismatches 35; Indels 2; Gaps 1;

OY 1 MFOQDERRRKLPOLCTELQTHIHDIIECYCKQOQLRREYDFAFRLDCTVYRDGNPY 60
DB 1 MFOQDERRRKLPOLCTELQTHIHDIIECYCKQOQLRREYDFAFRLDCTVYRDGNPY 60
OY 61 AVCDKCLAFKYSKYSERHRCYSLYGTTLEQYNNKPLCDLLIRINCQKPLCEKORHND 120
DB 61 AVCDKCLAFKYSKYSERHRCYSLYGTTLEQYNNKPLCDLLIRINCQKPLCEKORHND 120
OY 61 AVCKVCLRLSKISEYRHNYSLYGTLEQYNNKPLCDLLIRINCQKPLCEKORHND 120
DB 61 AVCKVCLRLSKISEYRHNYSLYGTLEQYNNKPLCDLLIRINCQKPLCEKORHND 120
OY 121 KKQRFNINGRWGTGRCMSCCRSSRTRETQL 151
DB 121 KKQRFNINGRWGTGRCACWRR--RRRTQL 149

RESULT 6
VE6_HPV52 STANDARD; PRT; 148 AA.
AC P36814;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE E6 protein.
GN E6.
OS Human papillomavirus type 52.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10618;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94265501; PubMed=8205838;
RA Delius H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC STRANDED DNA (IN VITRO).
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC
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DR EMBL: X74481; CAAS2585.1; -.
DR PIR: S36573; S36573.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
KM Early protein; DNA-binding; Nuclear protein; zinc-finger.
FT ZN_FING 30 66 POTENTIAL.
FT ZN_FING 103 139 POTENTIAL.
SQ SEQUENCE 148 AA; 17898 MW; C5E9DECE341ABDE CRC64;

Query Match
Best Local Similarity 59.6%; Score 507; DB 1; Length 148;
Matches 89; Conservative 18; Mismatches 34; Indels 0; Gaps 0;

OY 1 MFQDQPERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFARDCIYRDGNPY 60
DB 1 MFEDPAPRPTLHELCEVLESVEHRLQCQCKELQREYVKEFTDRIYRDNNPY 60
OY 61 AVDCIKLFYSKSEYRHVYCSLYGTTLEQYKPKLDCILRCINCKPLCPKPKORHL 120
DB 61 GVCIMCRLFLSKISEYRHVYCSLYGTTLEQYKPKLDCILRCINCKPLCPKPKERHVN 120
OY 121 KQRFHNRGRWTRGRCMSCR 141
DB 121 AKRFHNRGRWTRGRCSECR 141

RESULT 7
VE6_HPV34 STANDARD; PRT; 148 AA.
AC P36811;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE E6 protein.
GN E6.
OS Human papillomavirus type 34.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10613;
RN RP SEQUENCE FROM N.A.
RX MEDLINE=9425501; PubMed=8205838;
RA Deilus H., Hotmann B.;
RT Primer-directed sequencing of human papillomavirus types. ";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC STRANDED DNA (IN VITRO).
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.
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CC -----
DR EMBL: X74476; CAAS2555.1; -.
DR PIR: S36515; S36515.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
KM Early protein; DNA-binding; Nuclear protein; zinc-finger.
FT ZN_FING 31 67 POTENTIAL.
FT ZN_FING 104 140 POTENTIAL.
SQ SEQUENCE 148 AA; 17735 MW; E2FC6E62E4AFODA CRC64;

Query Match
Best Local Similarity 58.6%; Score 499; DB 1; Length 148;
Matches 88; Conservative 17; Mismatches 39; Indels 0; Gaps 0;

OY 2 FQDQPERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFARDCIYRDGNPY 61
DB 2 FQDQPERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFARDCIYRDGNPY 61
DB 3 FPNPDERPRKLPALCEVNISIHIEILDVYCEVDFIRFDLCVVRKPKLG 62

```

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OY 62 VCDCKLFYSKSEYRHVYCSLYGTTLEQYKPKLDCILRCINCKPLCPKPKORHL 121
DB 63 VQCPCLLFYSKSVGRYRNYNSVGRILENTLNQCLNILLRCCKCKPLCPLEKQHRVDE 122
OY 122 KQRFHNRGRWTRGRCMSCRSRT 145
DB 123 NKRPHQIADQWTRGTCQWRPSAT 146

RESULT 8
VE6_HPV70 STANDARD; PRT; 158 AA.
ID VE6_HPV70
AC P50804;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE E6 protein.
GN E6.
OS Human papillomavirus type 70.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=39457;
RN RP SEQUENCE FROM N.A.
RX MEDLINE=96249586; PubMed=8815087;
RA Forslund O., Hansson B.G.;
RT "Human papillomavirus type 70 genome cloned from overlapping PCR
RT products: complete nucleotide sequence and genomic organization.";
RL J. Clin. Microbiol. 34:802-809(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97060129; PubMed=8904450;
RA Longuet M., Beaudeau S., Orth G.;
RT "Two novel genital human papillomavirus (HPV) types, HPV68 and HPV70,
RT related to the potentially oncogenic HPV39.";
RL J. Clin. Microbiol. 34:738-744(1996).
CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC STRANDED DNA (IN VITRO).
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U21941; AAC54850.1; -.
DR EMBL: U22461; AAC54880.1; -.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
KM Early protein; DNA-binding; Nuclear protein; zinc-finger.
FT ZN_FING 32 68 POTENTIAL.
FT ZN_FING 105 141 POTENTIAL.
FT CONFICT 100 100 N -> D (IN REF. 2).
SQ SEQUENCE 158 AA; 18611 MW; 6B610800D923D6DE CRC64;

Query Match
Best Local Similarity 56.8%; Score 483.5; DB 1; Length 158;
Matches 89; Conservative 21; Mismatches 40; Indels 5; Gaps 1;

OY 2 FQDQPERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFARDCIYRDGNPY 61
DB 4 FPNPDERPRKLPALCEVNISIHIEILDVYCEVDFIRFDLCVVRKPKLG 63
OY 62 VCDCKLFYSKSEYRHVYCSLYGTTLEQYKPKLDCILRCINCKPLCPKPKORHL 121
DB 64 ACQCKLIFAKVAKELRHSYSVATITLESITNNKLNLSRCSCLKPLCPAKLKHVNT 123
OY 122 KQRFHNRGRWTRGRCMSCRS-----RTRETEL 151

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91303675; PubMed=1649326;
RA Lungu O., Crum C.P., Silverstein S.J.;
RT "Biologic properties and nucleotide sequence analysis of human
RL papillomavirus type 51."
CC J. Virol. 65:4216-4225(1991).
CC -I- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC STRANDED DNA (IN VITRO).
CC CC -I- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC CC
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CC -----
DR EMBL; M62877; -. NOT_ANNOTATED_CDS.
DR PIR; E40415; W6WL51.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR KW Early protein; DNA-binding; Nuclear protein; Zinc-finger.
FT ZN_FING 30 66 POTENTIAL.
FT ZN_FING 103 139 POTENTIAL.
SQ SEQUENCE 151 AA; 18134 MW; 577E63BA1376478 CRC64;

Query Match 55.7%; Score 474; DB 1; Length 151;
Best Local Similarity 57.0%; Pred. No. 1e-38;
Matches 86; Conservative 25; Mismatches 40; Indels 0; Gaps 0;

QY 1 MEODPQERPRRLPOLCTELQTTHIDILECYCKQQLRREYVDFAFRDLCIVYRDGPNY 60
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1 MFEDRKREPRRLHELCEALNVSMHNIGYGVYCKKELCRADYVNNAFLEIKVIYVDNNPY 60

QY 61 AVCDKCLKFYSKYSTRNYHCYSLYGTTEEQYNKPLCDLLRCINCQKPLDPEEKQRHD 120
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 61 AVCCKCLEFYSKIRRYRSRVYGTTLTAITKSLYDLISIRCHCQRPDLPDEEKOKLD 120

QY 121 KKORFNHRIGRWTCRCMCSRSSRRPRETOI 151
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 121 EKRFHELAGHWIGOCANCWQTRORNETQV 151

RESULT 11
VE6_HPV45 STANDARD: PRT: 158 AA.
AC P21735.
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE E6 protein.
E6.
GN Human papillomavirus type 45.
OS Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10593;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94265501; Pubmed=8205838;
RA Delius H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
CC CC
CC CC SEQUENCE FROM N.A.
CC RA Kaplan J.B., Burk R.D.;
CC Submitted (AUG-1990) to the EMBL/Genbank/DDBJ databases.
CC -I- FUNCTION: THIS PROTEIN HAS TRANSFORMING ACTIVITY IN VITRO.
CC CC -I- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC STRANDED DNA (IN VITRO).
CC CC -I- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC -----

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X74479; CAA52573.1; -
DR EMBL: M38198; AAA46973.1; -
DR PIR: S36561; S36561
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
KW Early protein; DNA-binding; Nuclear protein; Zinc-finger;
KW Oncogene.
FT ZN_FING 32 68 POTENTIAL.
FT ZN_FING 105 141
FT CONFLICT 10 10 R->P (IN REF. 2).
FT CONFLICT 30 30 I->N (IN REF. 2).
FT CONFLICT 118 118 R->A (IN REF. 2).
SQ SEQUENCE 158 AA; 18897 MW; FICF10DD33AA4C3E CRC64;

Query Match 55.6%; Score 473.5; DB 1; Length 158;
Best Local Similarity 56.1%; Pred. No. 1.2e-38;
Matches 87; Conservative 23; Mismatches 40; Indels 5; Gaps 1;

OY 2 FODPQERPRKLPOLCTELQTTIHDIIECYVCKOOLLRRREYDFAFDLCIVRDGNPYA 61
DB 4 FDDPQRRRYKLPDLCTELNTSLQDIETCYVCKATLETFEYGFARFQKLCIVRDCINVA 63
OY 62 VCDKCLAFYSKYSERYHRCYSLSYGTTLBEOQYNKPLCDLLIRNCINQKPLCPCEKORHLDK 121
DB 64 ACHNCIDFYSRIRLEIRYSNSVGETLEKINTLEYNLLIRCLRCQKPLNPAEKRRHLKD 123

OY 122 KQRFHNRGRMTGRCMCCRSS-----RTREPOL 151
DB 124 KRREHNIAGHYRGCHSCCNRAQERLRRLRRRETQV 158

RESULT 12
VE6_HPVI8
ID VE6_HPVI8 STANDARD; PRT; 158 AA.
AC P06463;
DT 01-JAN-1988 (Rel. 06, Created)
DT 15-JUN-2002 (Rel. 06, Last sequence update)
DE E6 protein.
GN E6
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=67283882; Pubmed=3039146;
RA Cole S.T., Danos O.;
RT "Nucleotide sequence and comparative analysis of the human
RT papillomavirus type 18 genome. Phylogeny of papillomaviruses and
RT repeated structure of the E6 and E7 gene products.";
RL J. Mol. Biol. 193:599-608(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=6630665; Pubmed=3018129;
RA Malahowski G., Banks L., Wu-Liao J., Spence P., Pim D., Crawford L.;
RT "The expression of human papillomavirus type 18 E6 protein in
RT bacteria and the production of anti-E6 antibodies.";
RL J. Gen. Virol. 67:1909-1916(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88188247; Pubmed=2833614;
RA Terada M., Sugimura T.; Takebe N., Nawa H., Nakanishi S.;
RT "Nucleotide sequences of cDNAs for human papillomavirus type 18

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RT transcripts in HeLa cells.";
RL J. Virol. 62:1640-1646(1988).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=67053870; Pubmed=3023067;
RA Schneider-Gaedicke A., Schwarz E.;
RT "Different human cervical carcinoma cell lines show similar
RT transcription patterns of human papillomavirus type 18 early genes.";
RL EMO J. 5:2285-2292(1986).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=67218459; Pubmed=3034571;
RA Seedorf K., Oltersdorf T., Kraemer G., Roewekamp W.;
RT "Identification of early proteins of the human papilloma viruses type
RT 16 (HPV 16) and type 18 (HPV 18) in cervical carcinoma cells.";
RL EMO J. 6:139-144(1987).
RN [6]
RP ZINC-BINDING.
RX MEDLINE=69385606; Pubmed=2550872;
RA Grossman S.R., Laimins L.A.;
RT "E6 protein of human papillomavirus type 18 binds zinc.";
RL Oncogene 4:1089-1093(1989).
CC -1- FUNCTION: THIS PROTEIN HAS TRANSFORMING ACTIVITY IN VITRO.
CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC STRANDED DNA (IN VITRO).
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.
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CC -----
DR EMBL: X04354; CAA27879.1; -
DR EMBL: X05015; CAA28664.1; -
DR EMBL: M20325; AAA99514.1; -
DR EMBL: M26798; AAA46946.1; -
DR EMBL: X04773; CAA28466.1; -
DR EMBL: A06324; CAA00539.1; -
DR EMBL: A06328; CAA00542.1; -
DR PIR: G26251; W6WL18.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
KW Early protein; DNA-binding; Nuclear protein; Zinc-finger;
KW Oncogene.
FT ZN_FING 32 68 POTENTIAL.
FT ZN_FING 105 141
FT CONFLICT 22 22 N->S (IN REF. 4).
SQ SEQUENCE 158 AA; 18871 MW; 5BCF13CP43D157FA CRC64;

Query Match 55.2%; Score 469.5; DB 1; Length 158;
Best Local Similarity 56.1%; Pred. No. 2.9e-38;
Matches 87; Conservative 22; Mismatches 41; Indels 5; Gaps 1;

OY 2 FODPQERPRKLPOLCTELQTTIHDIIECYVCKOOLLRRREYDFAFDLCIVRDGNPYA 61
DB 4 FEDTTRRYKLPDLCTELNTSLQDIETCYVCKATLETFEYGFARFQKLCIVRDCINVA 63
OY 62 VCDKCLAFYSKYSERYHRCYSLSYGTTLBEOQYNKPLCDLLIRNCINQKPLCPCEKORHLDK 121
DB 64 ACHNCIDFYSRIRLEIRYSNSVGETLEKINTLEYNLLIRCLRCQKPLNPAEKRRHLNE 123

OY 122 KQRFHNRGRMTGRCMCCRSS-----RTREPOL 151
DB 124 KRREHNIAGHYRGCHSCCNRAQERLRRLRRRETQV 158

RESULT 13
VE6_HPVI8
ID VE6_HPVI8 STANDARD; PRT; 158 AA.
AC P27962;

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DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE E6 protein.
GN E6.
OS Human papillomavirus type ME180.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91374616; PubMed-1716694;
RA Reuter S., Delius H., Kahn T., Hofmann B., Zur Hausen H., Schwarz E.;
RT "Characterization of a novel human papillomavirus DNA in the cervical
RT carcinoma cell line ME180."
RT J. Virol. 65:5564-5568(1991).
CC -!- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC -!- STRANDED DNA (IN VITRO).
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
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CC -----
CC EMBL: M73258; -, NOT_ANNOTATED_CDS.
CC DR PIR: C40509; W6WLP.
CC DR InterPro: IPR001334; E6.
CC DR Pfam: PF00518; E6; 1.
CC KM Early protein: DNA-binding; Nuclear protein; Zinc-finger.
CC FT ZN_FING 32 68 POTENTIAL.
CC FT ZN_FING 106 141 POTENTIAL.
CC SQ SEQUENCE 158 AA; 18738 MW; 2B1F406B563F05FC CRC64;

Query Match
Best Local Similarity 54.7%; Score 465.5; DB 1; Length 158;
Matches 86; Conservative 22; Mismatches 43; Indels 5; Gaps 1;

OY 1 MFQDPQERPRKLPQCTELQTTIHDIILCEVCYKQOQLRREYDFAFRDLCTIYRDGNPY 60
DB 3 LFHNPEERPRKLPDLCRTLDITLHDVITDVCYCRRLQRTVEYEFAGDLNLYYRGVPL 62
OY 61 AVCDKLTFRYSKYSEYRHYCYSLYGTTLDEQYKPLCDLLIRINCQKPLCPBEKORHDK 120
DB 63 AACQSCIKFYAKTRELRYSESYVATLTITNTKLYDISIRCMCLKPLSPAETKLRLHN 122
OY 121 KROFHNIRGRTGRCMSCCRSSR-----TRRRETOL 151
DB 123 SKRRFKIAGNFTGCCRHCWTSKREDRRRLRRETQV 158

RESULT 14
VE6_HPV39
ID VE6_HPV39 STANDARD; PRT; 158 AA.
AC P24835;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE E6 protein.
GN E6.
OS Human papillomavirus type 39.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10588;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91135017; PubMed-1847266;
RA Volpers C., Strebeck R.E.;
RT "Genome organization and nucleotide sequence of human papillomavirus
RT type 39."

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RL Virology 181:419-423(1991).
CC -!- FUNCTION: THIS PROTEIN MAY BE INVOLVED IN THE ONCOGENIC POTENTIAL
CC OF THIS VIRUS (CERVICAL NEOPLASIA-ASSOCIATED VIRUS).
CC -!- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC -!- STRANDED DNA (IN VITRO).
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC -----
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CC -----
CC EMBL: M62849; AAA47050.1; -.
CC DR PIR: A38502; W6WLP39.
CC DR InterPro: IPR001334; E6.
CC DR Pfam: PF00518; E6; 1.
CC KM Early protein: DNA-binding; Nuclear protein; Zinc-finger;
CC KM Oncogene.
CC FT ZN_FING 32 68 POTENTIAL.
CC FT ZN_FING 105 141 POTENTIAL.
CC SQ SEQUENCE 158 AA; 18726 MW; 1B5E9D55BC1B662E CRC64;

Query Match
Best Local Similarity 54.5%; Score 463.5; DB 1; Length 158;
Matches 86; Conservative 20; Mismatches 44; Indels 5; Gaps 1;

OY 2 FQDPQERPRKLPQCTELQTTIHDIILCEVCYKQOQLRREYDFAFRDLCTIYRDGNPYA 61
DB 4 FHNPARPRKLPDLCRTLDITLHDVITDVCYCRRLQRTVEYEFAGDLNLYYRGVPLA 63
OY 62 VCDCKLTFYSKYSEYRHYCYSLYGTTLDEQYKPLCDLLIRINCQKPLCPBEKORHDK 121
DB 64 AACQSCIKFYAKTRELRYSESYVATLTITNTKLYDISIRCMCLKPLSPAETKLRLHN 123
OY 122 KROFHNIRGRTGRCMSCCRSSR-----TRRRETOL 151
DB 124 KRRFKIAGSYTGCCRHCWTSKREDRRRLRRETQV 158

RESULT 15
VE6_RHPV1
ID VE6_RHPV1 STANDARD; PRT; 191 AA.
AC P22159;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE E6 protein.
GN E6.
OS Rhesus papillomavirus type 1 (Rhpv 1).
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10570;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91135018; PubMed-1847267;
RA Ostrow R.S., Labresh K.V., Faras A.J.;
RT "Characterization of the complete Rhpv 1 genomic sequence and an
RT integration locus from a metastatic tumor."
RT Virology 181:424-429(1991).
CC -!- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC -!- STRANDED DNA (IN VITRO).
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC -----
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CC	EMBL	60184	AA79311.1	-
DR	PIR	A38503	W6WRL	
DR	InterPro	IPR001334	E5	
DR	Pfam	PF00518	E5	1
KW	Family protein	DNA-binding	Nuclear Protein	zinc-finger
FT	2N_FING	60	96	POTENTIAL
FT	ZN_FING	133	169	POTENTIAL
SO	SEQUENCE	191	AA: 22701	MM: F819CF89452B90D CRC64

Query Match	53.3%	Score 454;	DB 1;	Length 191;
Best Local Similarity	56.5%	Pred. No. 1.1e-36;		
Matches	83;	Conservative	23;	Mismatches 39;
			Indels	2;
			Gaps	1;

```

0Y 4 DPOEPRRLPOLCJHELQTTIHDIILCEYKQOOLREBYVDFAFRDICIYUROPNGPRAWC 63
Db 34 EPNELPRITHLCEORETTHLEHIDECYUJLCKELTRLEVYDFAMWDLVLRHOKRPGWC 93
0Y 64 DKCLKFSKYSEYRNYHCYSLGTGLLEOYVNPRLCDLLIRICINCOPLCPREKORHLDIKQ 123
Db 94 PCLRFYFIRKIRRYEYSITGCTLLERTRKQVLVEILRICYCCOKPLCPREKORHNDQOQ 153
0Y 124 RFHNIRGWTGRCSGCCSSRTRRETQ 150
Db 154 RFHNRAGOWTGRCLCMQRP--TVETQ 178

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Search completed: December 13, 2002, 08:38:38
Job time : 16.7485 secs
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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 13, 2002, 08:36:45 ; Search time 24.0859 Seconds

(without alignments)  
602.689 Million cell updates/sec

Title: US-09-701-080C-18

Perfect score: 851

Sequence: 1 MFDDPERPKRLPOLCTELQ.....WTGRCMSCCRSSRRTRRQL 151

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	843	99.1	158	1 W6WLIHS	protein E6 - human
2	592	69.6	149	1 W6WLI35	E6 protein - human
3	538	63.2	149	1 W6WLI31	E6 protein - human
4	534	62.7	149	1 W6WLI33	E6 protein - human
5	516	60.6	149	1 W6WLI58	E6 protein - human
6	507	59.6	148	2 A61237	E6 protein - human
7	507	59.6	148	2 S36573	E6 protein - human
8	499	58.6	148	2 S36515	E6 protein - human
9	474	55.7	151	1 W6WLI51	E6 protein - human
10	473.5	55.6	158	2 S36561	E6 protein - human
11	469.5	55.2	158	1 W6WLI18	E6 protein - human
12	465.5	54.7	158	1 W6WLI39	E6 protein - human
13	463.5	54.5	158	1 W6WLI39	E6 protein - human
14	454.5	53.3	191	1 W6WLI31	E6 protein - human
15	450.5	52.9	150	2 S36544	E6 protein - human
16	441.5	51.9	155	1 W6WLI56	E6 protein - human
17	406.5	47.8	153	2 S36503	E6 protein - human
18	394	46.3	154	2 S36527	E6 protein - human
19	387.5	45.5	155	2 A44890	E6 protein - human
20	342.5	40.2	155	2 W6WLI43	E6 protein - human
21	332	37.8	153	1 S15621	E6 protein - human
22	320	37.6	150	1 W6WLI6	E6 protein - human
23	318	37.4	150	1 W6WLI44	E6 protein - human
24	316.5	37.2	159	2 S15614	E6 protein - human
25	311	36.5	159	2 S36497	E6 protein - human
26	310	36.4	150	1 W6WLI11	E6 protein - human
27	307.5	36.1	154	2 S36584	E6 protein - human
28	305.5	35.9	154	2 S36555	E6 protein - human
29	305	35.8	150	1 W6WLI1	E6 protein - human

30	300	35.3	142	2 S36509	E6 protein - human
31	289	34.0	150	1 W6WLI3	E6 protein - human
32	284	33.4	150	1 W6WLI42	E6 protein - human
33	257	30.2	148	2 S36532	E6 protein - human
34	252	29.6	152	2 S36550	E6 protein - human
35	182	21.4	138	2 S36567	E6 protein - human
36	170.5	20.0	141	2 S36479	E6 protein - human
37	156	18.3	156	1 W6WLI41	E6 protein - human
38	155.5	18.3	140	1 W6WLI	E6 protein - human
39	154	18.1	161	2 S36491	E6 protein - human
40	150.5	17.7	139	1 W6WLI2	E6 protein - human
41	150.5	17.7	141	2 S36473	E6 protein - human
42	150	17.6	157	2 S36538	E6 protein - human
43	148.5	17.5	207	2 S28510	E6 protein - human
44	146	17.2	156	1 W6WLI47	E6 protein - human
45	145	17.0	166	2 S36485	E6 protein - human

#### ALIGNMENTS

##### RESULT 1

W6WLIHS  
protein E6 - human papillomavirus type 16  
C:Species: human papillomavirus type 16  
C:Date: 28-May-1986 #sequence\_revision 28-May-1986 #text\_change 20-Aug-1999  
C:Accession: A03682; T10427  
R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Roweckamp, W.G.  
Virology 145, 181-185, 1985  
A:Title: Human papillomavirus type 16 DNA sequence.  
A:Reference number: A22355; MUID:85246220; PMID:2990099  
A:Accession: A03682  
A:Molecule type: DNA  
A:Residues: 1-158 <SEQ>  
A:Cross-references: GB:K02718; NID:9333031; PIDN:AAA46939.1; PID:9333032  
R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.  
J. Virol. 65, 2093-2097, 1991  
A:Title: A negative element in the human poapillomavirus type 16 genome acts at the 1  
A:Reference number: 217014; MUID:91162763; PMID:1848319  
A:Accession: T10427  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-158 <KEN>  
A:Cross-references: EMBL:K02718; NID:9333031; PIDN:AAA46939.1; PID:9333032  
C:Genetics:  
A:Gene: E6  
C:Superfamily: papillomavirus E6 protein  
C:Keywords: DNA binding; early protein; zinc finger  
F:37-73/Region: zinc finger CCCC motif  
F:110-146/Region: zinc finger CCCC motif

Query Match 99.1%; Score 843; DB 1; Length 158;  
Best Local Similarity 99.3%; Pred. No. 8.3e-69;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFDDPERPKRLPOLCTELQTHDILTCVCKQOLLREVDFAFRDICTVYRGPNY 60  
|||||  
Db 8 MFDDPERPKRLPOLCTELQTHDILTCVCKQOLLREVDFAFRDICTVYRGPNY 67  
|||||

QY 61 AVCDKLKFKYSKSEYRHCYSLYGTTLEQYKRPICDILIRICINQKPLCPKXORHND 120  
|||||  
Db 68 AVCDKLKFKYSKSEYRHCYSLYGTTLEQYKRPICDILIRICINQKPLCPKXORHND 127  
|||||

QY 121 KKQRFNINRGWTCRCMSCCRSSRRTRRQL 151  
|||||  
Db 128 KKQRFNINRGWTCRCMSCCRSSRRTRRQL 158  
|||||

RESULT 2  
W6WLI35  
E6 protein - human papillomavirus type 35  
C:Species: human papillomavirus type 35  
A:Note: host Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Mar-2001  
C:Accession: E40824; S36521  
R:Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.  
Virology 186, 770-776, 1992  
A:Title: The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 18  
A:Reference number: A40824; MUID:92124753; PMID:1310198  
A:Accession: E40824  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-149 <MAR>  
A:Cross-references: GB:W14117; NID:g333050; PIDN:AAA4696.1; PID:g333051  
R:Delius, H.; Hofmann, B.  
submitted to the EMBL Data Library, August 1993  
A:Description: Primer-directed sequencing of human papillomavirus types.  
A:Reference number: S36469  
A:Accession: S36521  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-149 <DEL>  
A:Cross-references: EMBL:X74477; NID:g396997; PIDN:CAA52561.1; PID:g396998  
A:Experimental source: strain 35H  
C:Superfamily: papillomavirus B6 protein  
C:Keywords: DNA binding; early protein; zinc finger  
F:30-66/Region: zinc finger CCCC motif  
F:103-139/Region: zinc finger CCCC motif

Query Match	69.6%	Score 592	DB 1	Length 149
Best Local Similarity	71.5%	Pred. No. 2.9e-46		
Matches 108	Conservative 14	Mismatches 27	Indels 2	Gaps 1
QY	1	MFQDQERPRKLPQCTLETQTTIHDIILECVYCKQOLLRREYDEAFNRDCLIVRGDNPY	60	
		: : :   :   :   :   :   :   :   :   :   :   :   :   :		
Db	1	MFQDAERPRYKXHDLCNVEEESIHETCLNVCYCKDELQRESEYDPRACYDCLIVREGQY	60	
QY	61	AVCDKCLKFFSYSEYSEYRHVYSLVGTTLEQQYKPKLDLILRCINCQKPLCEEKQRIID	120	
Db	61	GVCMCKLKFYSKISEYRWYRSYVGETLEKQNKQDLCHILIRCINCQKPLCEVEKQRIHE	120	
QY	121	KKQRFHNIRGRWTGRCMSCCRSSRRRERQQL	151	
		: : :                   : : :		
Db	121	EKKRFHNIRGRWTGRCMSCMRP--TRRETEV	149	

RESULT 3  
W6M131  
E6 protein - human papillomavirus type 31  
C:Species: human papillomavirus type 31  
A>Note: host Homo sapiens (nan)  
C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 16-Jul-1999  
C:Accession: A32444  
R:Goldsbrough, M.D.; Dislyestre, D.; Temple, G.F.; Lorincz, A.T.  
Virology 171: 306-311, 1989  
A:Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associated  
A:Reference number: A94398; MUID:89299478; PMID:2545036  
A:Accession: A32444  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-149 <GOI>  
A:Cross-references: GB:J04353; NID:q333048; PIDN:AAA4650.1; PID:q459916  
C:Comment: This protein may be involved in the oncogenic potential of this virus.  
C:Superfamily: Papillomavirus E6 protein  
C:Keywords: DNA binding; early protein; zinc finger  
#:30-66/Region: zinc finger CCCC motif  
#:103-139/Region: zinc finger CCCC motif

```

Query Match 1: Score 538; DB 1; Length 149;
Best Local Similarity 65.6%; Pred. No. 2,1e-41;
Matches 99; Conservative 18; Mismatches 33; Indels 2; Gaps 1;

QY 1 MFQDQERRKILPOLCTELQTTIHDIILCEYCKKQQLRREYDFAFRDLCTIVYDGNFY 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MKNAEPRKRIHETSSALEIETPYDELRLNVCYCKQLTEYELDAIFADTLTVYRDDPH 60

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[illegible]

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RESULT 4
M6ML3
E6 protein - human papillomavirus type 33
C:Species: human papillomavirus type 33
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
C:Accession: A03683
R:Cole, S.T.; Strebeck, R.E.
J. Virol. 58, 991-995, 1986
A:Title: Genome organization and nucleotide sequence of human papillomavirus type 33.
A:Reference number: A93020; MUID:86200464; PMID:3009902
A:Accession: A03683
A:Molecule type: DNA
A:Residues: 1-149 <COL>
A:Cross-references: GB:M2732; NID:q3335049; PIDD:AAA46558.1; PID:q463177
C:Superfamily: Papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

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	Query Match	62.7%	Score 534;	DB 1:	Length 149;
	Best Local Similarity	63.6%;	Pred. NO. 4.8e-41;		
	Matches	96;	Conservative	20;	Mismatches 33; Indels 2; Gaps 1;
OY	1 MFQDQERPRKLPOLCTELQTTHDIILCEVCCKOOLLREVEYDEAFRLDJCIYVRGDNPY	60			
Dd	1 MFDIIEEKRPTLHDCQALETTHIHNIQCVCBCKPLQRSEVYDAFADLTYYVEGNFF	60			
OY	61 AYCDKCLAFYSKYSEYRHYSCLVGTTLEQOYNKPLCDLLIRICINQPKPLCEEKORHL	120			
Dd	61 GICKLCLEFLSKISSEYRHHNYSVYGNTLEQYKKPRLNETLIRICIQLCPQEKRRHD	120			
OY	121 KKQFHNTIRGWTCGRMCSGCRSRRRREFQL	151			
Dd	121 LNRKPHNISGRWAGCAACWRs--RRRETAL	149			

```

RESULT 5
W6WL58
E6 protein - human papillomavirus type 58
C:Species: human papillomavirus type 58
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jul-2000
C:Accession: E36779
R:Kiril, Y.; Iwamoto, S.; Matsukura, T.
Virology 185, 424-427, 1991
A:Title: Human papillomavirus type 58 DNA sequence.
A:Reference number: A36779; MUID:92024102; PMID:1656594
A:Accession: E36779
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-149 <RIR>
A:Cross-references: GB:090400; NID:9222386; PIDN:BA31845.1; PID:g3337098
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

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[illegible]









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